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(54) Title: COMPOSITIONS FROM THE GRASSES *LOLIUM PERENNE* AND *FESTUCA ARUNDINACEA*

(57) Abstract: Isolated polynucleotides encoding polypeptides from *Lolium perenne* and *Festuca arundinacea* active in lignin, fructan and tannin biosynthetic pathways are provided, together with expression vector and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

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Compositions from the grasses *Lolium perenne* and *Festuca arundinacea*.

COMPOSITIONS ISOLATED FROM FORAGE GRASSES AND METHODS FOR THEIR USE

Reference to Related Applications

This application claims priority to U.S. Provisional Patent Application No. 60/337,703 filed November 7, 2001.

Technical Field of the Invention

This invention relates to polynucleotides isolated from forage grass tissues, specifically from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue), as well as oligonucleotide probes and primers, genetic constructs comprising the polynucleotides, biological materials (including host cells and plants) incorporating the polynucleotides, polypeptides encoded by the polynucleotides, and methods for using the polynucleotides and polypeptides. More particularly, the invention relates to polypeptides involved in the lignin, tannin and fructan biosynthetic pathways, and to polynucleotides encoding such polypeptides.

Background of the Invention

Over the past 50 years, there have been substantial improvements in the genetic production potential of ruminant animals (sheep, cattle and deer). Levels of meat, milk or fiber production that equal an animal's genetic potential may be attained within controlled feeding systems, where animals are fully fed with energy dense, conserved forages and grains. However, the majority of temperate farming systems worldwide rely on the *in situ* grazing of pastures. Nutritional constraints associated with temperate pastures can prevent the full expression of an animal's genetic potential. This is illustrated by a comparison between milk production by North American grain-fed dairy cows and New Zealand pasture-fed cattle. North American dairy cattle produce, on average, twice the milk volume of New Zealand cattle, yet the genetic base is similar within both systems (New Zealand Dairy Board and United States Department of Agriculture figures). Significant potential therefore exists

to improve the efficiency of conversion of pasture nutrients to animal products through the correction of nutritional constraints associated with pastures.

Lignin Biosynthetic Pathway

Lignin is an insoluble polymer that serves as a matrix around the polysaccharide components of some plant cell walls, and that is primarily responsible for the rigidity of plant stems. Generally, the higher the lignin content, the more rigid the plant. For example, tree species synthesize large quantities of lignin, with lignin constituting 20%-30% of the dry weight of wood. The lignin content of grasses ranges from 2-8% of dry weight and changes during the growing season. In addition to providing rigidity, lignin aids in water transport within plants by rendering cell walls hydrophobic and water impermeable. Lignin also plays a role in disease resistance of plants by impeding the penetration and propagation of pathogenic agents.

Forage digestibility is affected by both lignin composition and concentration. Lignin is largely responsible for the digestibility, or lack thereof, of forage crops, with small increases in plant lignin content resulting in relatively high decreases (> 10%) in digestibility (Buxton and Russell, *Crop. Sci.* 28:5358-558, 1988). For example, crops with reduced lignin content provide more efficient forage for cattle, with the yield of milk and meat being higher relative to the amount of forage crop consumed. During normal plant growth, an increase in the maturity of the plant stem is accompanied by a corresponding increase in lignin content and composition that causes a decrease in digestibility. This change in lignin composition is to one of increasing syringyl:guaiacyl (S:G) ratio. When deciding on the optimum time to harvest forage crops, farmers must therefore choose between a high yield of less digestible material and a lower yield of more digestible material.

Lignin is formed by polymerization of three different monolignols, *para*-coumaryl alcohol, coniferyl alcohol and sinapyl alcohol, that are synthesized in a multistep pathway, with each step in the pathway being catalyzed by a different enzyme. The three monolignols are derived from phenylalanine or tyrosine in a multistep process and are then polymerized into lignin by a free radical mechanism. Following polymerization, *para*-coumaryl alcohol, coniferyl alcohol and sinapyl alcohol are converted into the *p*-hydroxyphenyl (H), guaiacyl (G) and syringyl (S) units of lignin, respectively. While these three types of lignin subunits

are well known, it is likely that slightly different variants of these subunits may be involved in the lignin biosynthetic pathway in various plants. For example, studies suggest that both free monolignols and monolignol-4-coumarate esters may be substrates for lignin formation in grasses. The relative concentration of the monolignol residues in lignin varies among different plant species and within species. For example, the monolignol content for H/G/S of grasses, alfalfa and softwood gymnosperms is 22%/44%/34%, 7%/39%/54% and 14%/80%/6%, respectively (van Soest in "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY). The composition of lignin may also vary among different tissues within a specific plant.

Coniferyl alcohol, *para*-coumaryl alcohol and sinapyl alcohol are synthesized by similar pathways (Whetten *et al.*, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:585-609, 1998; Guo *et al.*, *Plant Cell* 13:73-88, 2001). The first step in the lignin biosynthetic pathway is the deamination of phenylalanine or tyrosine by phenylalanine ammonia-lyase (PAL) or tyrosine ammonia-lyase (TAL), respectively. In maize, the PAL enzyme also has TAL activity (Rosler *et al.*, *Plant Physiol.* 113:175-179, 1997). The product of TAL activity on tyrosine is 4-coumarate, whereas the product of PAL activity on phenylalanine is cinnamate which is then hydroxylated by cinnamate 4-hydroxylase (C4H) to form 4-coumarate. 4-Coumarate is hydroxylated by coumarate 3-hydroxylase (C3H) to give caffeate. The newly added hydroxyl group is then methylated by caffeic acid O-methyl transferase (COMT) to give ferulate. Several other methylation reactions can be catalyzed by COMT, including caffeoylaldehyde to coniferaldehyde, and 5-hydroxyconiferaldehyde to sinapaldehyde. 4-Coumarate, caffeate and ferulate can all be conjugated to coenzyme A by 4-coumarate:CoA ligase (4CL) to form 4-coumaryl CoA, caffeoyl CoA and feruloyl CoA, respectively. Caffeoyl CoA can then be methylated by the enzyme caffeoyl-CoA O-methyl transferase (CAMT).

Coniferaldehyde is hydroxylated to 5-hydroxyconiferaldehyde by ferulate 5-hydroxylase (F5H). Reduction of 4-coumaryl CoA, caffeoyl CoA and feruloyl-CoA to 4-coumaraldehyde, caffeoyl aldehyde and coniferaldehyde, respectively, is catalyzed by cinnamoyl-CoA reductase (CCR). Coumaraldehyde, caffeoyl aldehyde, coniferaldehyde and 5-hydroxyconfieraldehyde are further reduced by the action of cinnamyl alcohol dehydrogenase (CAD) to give coniferyl alcohol which is then converted into its glucosylated

form for export from the cytoplasm to the cell wall by coniferol glucosyl transferase (CGT). Recently a sinapyl alcohol dehydrogenase (SAD) was described that converts sinapaldehyde to sinapyl alcohol (Li *et al.*, *Plant Cell* 13:1567-1586, 2001). Following export, the de-glucosylated form of coniferyl alcohol is obtained by the action of coniferin *beta*-glucosidase (CBG). Finally, polymerization of the three monolignols to provide lignin is catalyzed by phenolase (PNL), laccase (LAC) and peroxidase (PER). For a more detailed review of the lignin biosynthetic pathway, *see* Whetton R and Sederoff R, *The Plant Cell*, 7:1001-1013, 1995 and Whetten *et al.*, *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:585-609, 1998.

Both lignin levels and composition have been changed in a range of plant species by altering the expression of specific lignin biosynthetic enzymes. For example, anti-sense 4CL constructs in transgenic aspen trees reduced lignin content from 20 to 11% (a 45% reduction) but at the same time increased both cellulose levels (by 15%) and growth rate (Hu *et al.* *Nature Biotechnol.* 17:808-812, 1999). These trees had the same level of total carbon, suggesting that carbon partitioning had been altered. Reducing 4CL by either anti-sense or sense-suppression in tobacco plants led to an accumulation of hydroxycinnamic acids in cell walls as well as a reduction in both guaiacyl and syringyl lignin units (Kajita *et al.*, *Plant Cell. Physiol.* 37:957-965, 1996). In transgenic tobacco plants in which levels of C4H were reduced by anti-sense or sense suppression, total lignin content was reduced, in addition to a reduction in syringyl lignin units (Sewalt *et al.*, *Plant Physiol.* 115:41-50, 1997). Reducing the levels of PAL in tobacco plants by anti-sense or sense-suppression reduced total lignin content but did not change the syringyl-guaiacyl (S:G) lignin ration. In alfalfa, reducing expression of COMT through either anti-sense or gene silencing decreased total lignin by decreasing the amount of guaiacyl units and resulted in a near total loss of syringyl lignin units (Guo *et al., Plant Cell* 13:73-88, 2001). In contrast, reducing CCOMT expression through anti-sense or gene silencing in alfalfa plants also decreased total lignin by reducing the total amount of guaiacyl lignin units but had no effect on the amount of syringyl lignin. Reducing CCR expression by anti-sense in tobacco plants resulted in reduced lignin content and increased S:G ratios due to lower guaiacyl lignin units (Piquemal *et al.*, *Plant J.* 13:71-83, 1998). *A. thaliana* plants where the F5H gene had been mutated contained only traces of syringyl lignin (Marita *et al.*, *Proc. Natl. Acad. Sci. USA* 96:12323-12332, 1999).

Alteration of grass lignin composition may usefully be employed to maintain high forage digestibility throughout the year. This is most important when the plant is approaching flowering and/or during flowering. At this time, the entire lignin biosynthetic pathway will preferably be reduced, in particular lowering the amount of syringyl lignin units, thereby lowering the S:G ratio and maintaining the digestibility of the forage crop.

Several of the enzymes involved in the lignin biosynthetic pathway also have other functions within the plant. For example, PAL is a key enzyme of plant and fungi phenylpropanoid metabolism and catalyzes the first step in phenylpropanoid metabolism. It is involved in the biosynthesis of a wide variety of secondary metabolites such as flavonoids, furanocoumar in phytoalexins and cell wall components. These compounds have many important roles in plants during normal growth and in responses to environmental stress. PAL catalyzes the removal of an ammonia group from phenylalanine to form trans-cinnamate.. PAL and the related histidine ammonia lyase are unique enzymes which are known to have the modified amino acid dehydroalanine (DHA) in their active site (Taylor *et al.*, *J. Biol. Chem.* 265:18192-18199, 1990). Phenylalanine and histidine ammonia-lyases (PAL) active site has a consensus of GTITASGDLVPLSYIA. The serine residue is central to the active site, and the region around this active site residue is well conserved (Langer *et al.*, *Biochem.* 33:6462-6467, 1994).

C4H, which is a member of the cytochrome P450 monooxygenase superfamily, plays a central role in both phenylpropanoid metabolism and lignin biosynthesis where it anchors a phenylpropanoid enzyme complex to the endoplasmic reticulum (ER). The phenylpropanoid pathway controls the synthesis of lignin, flower pigments, signaling molecules, and a large spectrum of compounds involved in plant defense against pathogens and UV light. This is also a branch point between general phenylpropanoid metabolism and pathways leading to various specific end products. 4CLs are a group of enzymes necessary for maintaining a continuous metabolic flux for the biosynthesis of plant phenylpropanoids, such as lignin and flavonoids that are essential to the survival of plants, because they serve important functions in plant growth and adaptation to environmental perturbations. Three isoforms of 4CL have been identified with distinct substrate preference and specificities. Expression studies in angiosperms revealed a differential behavior of the three genes in various plant organs and upon external stimuli such as wounding and UV irradiation or upon challenge with fungi.

One isoform is likely to participate in the biosynthetic pathway leading to flavonoids whereas the other two are probably involved in lignin formation and in the production of additional phenolic compounds other than flavonoids (Ehlting *et al.*, *Plant J.* 19:9-20, 1999).

F5H is involved in the phenylpropanoid biosynthesis pathway. It belongs to the CYP84 subfamily of the cytochrome P450 family and is known as cytochrome P450 84A1. F5H is one of the enzymes in the pathways leading to the synthesis of sinapic acid esters, but also has coniferaldehyde hydroxylase activity (Nair *et al.*, *Plant Physiol.* 123:1623-1634, 2000). In the generalized pathway for phenylpropanoid metabolism, F5H catalyzes the formation of 5-hydoxyferulate (a precursor of sinapate) and sinapate in turn as the precursor for sinapine and for sinapoyl CoA in two bifurcated pathways (Chapple *et al.*, *Plant Cell* 4:1413-1424, 1992). Sinapoyl CoA has been considered as the precursor for sinapyl alcohol, which is then polymerized into syringyl (S) lignin. In addition, CYP84 F5H product carries out the hydroxylation of coniferaldehyde (ConAld) to 5-OH ConAld (Nair *et al.*, *Plant Physiol.* 123:1623-1634, 2000).

Peroxidases are heme-containing enzymes that use hydrogen peroxide as the electron acceptor to catalyze a number of oxidative reactions. They belong to a superfamily consisting of 3 major classes. Class III consists of the secretory plant peroxidases, which have multiple tissue-specific functions in removal of hydrogen peroxide from chloroplasts and cytosol, oxidation of toxic compounds, biosynthesis of the cell wall, defense responses towards wounding, indole-3-acetic acid (IAA) catabolism and ethylene biosynthesis.

Fructan Biosynthetic Pathway

Plant carbohydrates can be divided into two groups depending on their function within the plant. Structural carbohydrates, such as cellulose, are usually part of the extracellular matrix. Non-structural, storage carbohydrates act as either long- or short-term carbohydrate stores. Examples of non-structural carbohydrates include starch, sucrose and fructans.

Fructans are polymers that are stored in the vacuole and that consist of linear and branched chains of fructose units (for review see Vijn and Smeekens *Plant Physiol.* 120:351-359, 1999). They play an important role in assimilate partitioning and possibly in stress tolerance in many plant families. Grasses use fructans instead of starch as a water-soluble

carbohydrate store (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.*, (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Increasing the amount of fructans and sucrose in forage crops leads to an increase in the level of water-soluble carbohydrates and thereby enhances the nutritional value of the plants. In addition, increasing the amount of fructans in forage plants decreases methane production in animals fed the plants, thereby leading to lower greenhouse gas emissions, and decreases urea production in animals as less protein is degraded in the rumen (Biggs and Hancock, *Trends in Plant Sci.* 6:8-9, 2001). Fructans have also been implicated in protecting plants against water deficits caused by drought or low temperatures. Introduction of enzymes involved in the fructan biosynthetic pathway into plants that do not naturally synthesize fructans may be employed to confer cold tolerance and drought tolerance (Pilon-Smits, *Plant Physiol.* 107:125-130, 1995).

The number of fructose units within a fructan chain is referred to as the degree of polymerization (DP). In grasses, fructans of DP 6-10 are common. Such fructans of low DP are naturally sweet and are therefore of interest for use as sweeteners in foodstuffs. Long fructan chains form emulsions with a fat-like texture and a neutral taste. The human digestive system is unable to degrade fructans, and fructans of high DP may therefore be used as low-calorie food ingredients. Over-expression of enzymes involved in the fructan biosynthetic pathway may be usefully employed to produce quantities of fructans that can be purified for human consumption.

Five major classes of structurally different fructans have been identified in plants, with each class showing a different linkage of the fructosyl residues. Fructans found in grasses are of the mixed levan class, consisting of both (2-1)- and (2-6)-linked beta-D-fructosyl units (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.*, (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Fructans are synthesized by the action of fructosyltransferase enzymes on sucrose in the vacuole. These enzymes are closely related to invertases, enzymes that normally hydrolyze sucrose.

Grasses use two fructosyltransferase enzymes to synthesize fructans, namely sucrose:sucrose 1-fructosyltransferase (1-SST) and sucrose:fructan 6-fructosyltransferase (6-SFT) (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et*

al., (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). 1-SST is a key enzyme in plant fructan biosynthesis, while 6-SFT catalyzes the formation and extension of beta-2,6-linked fructans that is typically found in grasses. Specifically, 1-SST catalyzes the formation of 1-kestose plus glucose from sucrose, while 6-SFT catalyzes the formation of bifurcose plus glucose from sucrose plus 1-kestose and also the formation of 6-kestose plus glucose from sucrose. Both enzymes can modify 1-kestose, 6-kestose and bifurcose further by adding additional fructose molecules. Over-expression of both 1-SST and 6-SFT in the same plant may be employed to produce fructans for use in human foodstuffs (Sevenier *et al.*, *Nature Biotechnol.* 16:843-846; Hellwege *et al.*, *Proc. Nat. Acad. Sci. USA* 97:8699-8704, 2000).

The synthesis of sucrose from photosynthetic assimilates in plants, and therefore the availability of sucrose for use in fructan formation, is controlled, in part, by the enzymes sucrose phosphate synthase (SPS) and sucrose phosphate phosphatase (SPP). Sucrose plays an important role in plant growth and development, and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression (for a review see Smeekens, *Curr. Opin. Plant Biol.* 1:230-234, 1998). SPS regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light (Huber *et al.*, *Plant Physiol.* 95:291-297, 1991). Specifically, SPS catalyzes the transfer of glucose from UDP-glucose to fructose-6-phosphate, thereby forming sucrose-6-phosphate (Suc-6-P). Suc-6-P is then dephosphorylated by SPP to form sucrose (Lunn *et al.*, *Proc. Natl. Acad. Sci. USA* 97:12914-12919, 2000). The enzymes SPS and SPP exist as a heterotetramer in the cytoplasm of mesophyll cells in leaves, with SPP functioning to regulate SPS activity. SPS is also important in ripening fruits, sprouting tubers and germinating seeds (Laporte *et al.*, *Planta* 212:817-822, 2001).

Once in the vacuole, sucrose can be converted into fructan by fructosyltransferases as discussed above, or hydrolyzed into glucose and fructose by the hydrolase enzymes known as invertases (Sturm, *Plant Physiol.* 121:1-7, 1999). There are several different types of invertases, namely extracellular (cell wall), vacuolar (soluble acid) and cytoplasmic, with at

least two isoforms of each type of invertase normally being found within a plant species. In addition to having different subcellular locations, the different types of invertases have different biochemical properties. For example, soluble and cell wall invertases operate at acidic pH, whereas cytoplasmic invertases work at a more neutral or alkaline pH. Invertases are believed to regulate the entry of sucrose into different utilization pathways (Grof and Campbell, *Aust. J. Plant Physiol.* 28:1-12, 2001). Reduced invertase activity may increase the level of water-soluble carbohydrates in plants. Plants contain several isoforms of cell wall invertases (CWINV), which accumulate as soluble proteins. CWINV plays an important role in phloem unloading and in stress response. It hydrolyzes terminal non-reducing beta-D-fructofuranoside residues in beta-D-fructo-furanosides.

Another enzyme that acts upon sucrose in plants is soluble sucrose synthase (SUS). Recent results indicate that SUS is localized in the cytosol, associated with the plasma membrane and the actin cytoskeleton. Phosphorylation of SUS is one of the factors controlling localization of the enzyme (Winter and Huber, *Crit. Rev. Biochem. Mol. Biol.* 35:253-89, 2000). It catalyzes the transfer of glucose from sucrose to UDP, yielding UDP-glucose and fructose. Increasing the amount of SUS in a plant increases the amount of cellulose synthesis, whereas decreasing SUS activity should increase fructan levels. Increased SUS concentration may also increase the yield of fruiting bodies. SUS activity is highest in carbon sink tissues in plants and low in photosynthetic source tissues, and studies have indicated that SUS is the main sucrose-cleaving activity in sink tissues. Grasses have two isoforms of SUS that are encoded by separate genes. These genes are differentially expressed in different tissues.

Tannin Biosynthetic Pathway

Condensed tannins are polymerized flavonoids. More specifically, tannins are composed of catechin 4-ol and catechin monomer units, and are stored in the vacuole. In many temperate forage crops, such as ryegrass and fescue, foliar tissues are tannin-negative. This leads to a high initial rate of fermentation when these crops are consumed by ruminant livestock, resulting in both protein degradation and production of ammonia by the livestock. These effects can be reduced by the presence of low to moderate levels of tannin. In certain other plant species, the presence of high levels of tannins reduces palatability and nutritive

value. Introduction of genes encoding enzymes involved in the biosynthesis of condensed tannins into a plant may be employed to synthesize flavonoid compounds that are not normally made in the plant. These compounds may then be isolated and used for treating human or animal disorders or as food additives.

Much of the biosynthetic pathway for condensed tannins is shared with that for anthocyanins, which are pigments responsible for flower color. Therefore, modulation of the levels of enzymes involved in the tannin biosynthetic pathway may be employed to alter the color of foliage and the pigments produced in flowers.

Most tannins described to date contain pro-cyanidin units derived from dihydroquercetin and pro-delphinidin units derived from dihydromyricetin. However, some tannins contain pro-pelargonidin units derived from dihydrokaempferol. The initial step in the tannin biosynthetic pathway is the condensation of coumaryl CoA with malonyl CoA to give naringenin-chalcone, which is catalyzed by the enzyme chalcone synthase (CHS). The enzyme chalcone isomerase (CHI) catalyzes the isomerization of naringenin chalcone to naringenin (also known as flavanone), which is then hydroxylated by the action of the enzyme flavonone 3- beta-hydroxylase (F3βH) to give dihydrokaempferol. The enzyme flavonoid 3'-hydroxylase (F3'OH) catalyzes the conversion of dihydrokaempferol to dihydroquercetin, which in turn can be converted into dihydromyricetin by the action of flavonoid 3'5'-hydroxylase (F3'5'OH). The enzyme dihydroflavonol-4-reductase (DFR) catalyzes the last step before dihydrokaempferol, dihydroquercetin and dihydromyricetin are committed for either anthocyanin (flower pigment) or proanthocyanidin (condensed tannin) formation. DFR also converts dihydrokaempferol to afzelchin-4-ol, dihydroquercetin to catechin-4-ol, and dihydromyricetin to gallocatechin-4-ol, probably by the action of more than one isoform. For a review of the tannin biosynthetic pathway, see, Robbins M.P. and Morris P. in Metabolic Engineering of Plant Secondary Metabolism, Verpoorte and Alfermann (eds), Kluwer Academic Publishers, the Netherlands, 2000.

While polynucleotides encoding some of the enzymes involved in the lignin, fructan and tannin biosynthetic pathways have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been identified.

Thus there remains a need in the art for materials useful in the modification of lignin, fructan and tannin content and composition in plants, and for methods for their use.

Summary of the Invention

The present invention provides enzymes involved in the lignin, fructan or tannin biosynthetic pathways that are encoded by polynucleotides isolated from forage grass tissues. The polynucleotides were isolated from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue) tissues taken at different times of the year, specifically in winter and spring, and from different parts of the plants, including: leaf blades, leaf base, pseudostems, floral stems, roots, inflorescences and stems. The present invention also provides genetic constructs, expression vectors and host cells comprising the inventive polynucleotides, and methods for using the inventive polynucleotides and genetic constructs to modulate the biosynthesis of lignins, fructans and tannins.

In specific embodiments, the isolated polynucleotides of the present invention comprise a sequence selected from the group consisting of: (a) SEQ ID NO: 1-62 and 125-162; (b) complements of SEQ ID NO: 1-62 and 125-162; (c) reverse complements of SEQ ID NO: 1-62 and 125-162; (d) reverse sequences of SEQ ID NO: 1-62 and 125-162; (e) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of (a)-(d), determined as described below; and (f) sequences having at least 75%, 80%, 90% or 98% identity to a sequence of (a)-(d), the percentage identity being determined as described below. Polynucleotides comprising at least a specified number of contiguous residues ("*x*-mers") of any of SEQ ID NO: 1-62 and 125-162; and oligonucleotide probes and primers corresponding to SEQ ID NO: 1-62 and 125-162 are also provided. All of the above polynucleotides are referred to herein as "polynucleotides of the present invention."

In further aspects, the present invention provides isolated polypeptides comprising an amino acid sequence of SEQ ID NO: 63-124 and 163-190, together with polypeptides comprising a sequence having at least 75%, 80%, 90% or 98% identity to a sequence of SEQ ID NO: 63-124 and 163-190, wherein the polypeptide possesses the same functional activity as the polypeptide comprising a sequence of SEQ ID NO: 63-124 and 163-190. The present invention also contemplates isolated polypeptides comprising at least a functional portion of a polypeptide comprising an amino acid sequence selected from the group consisting of: (a)

SEQ ID NO: 63-124 and 163-190; and (b) sequences having at least 75%, 80%, 90% or 98% identity to a sequence of SEQ ID NO: 63-124 and 163-190.

In another aspect, the present invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, in combination with one or more of the inventive sequences, or in combination with one or more known polynucleotides.

In certain embodiments, the present invention provides genetic constructs comprising, in the 5'-3' direction: a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. An open reading frame may be orientated in either a sense or anti-sense direction. Genetic constructs comprising a non-coding region of a polynucleotide of the present invention or a polynucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination sequences are functional in a host cell, such as a plant cell. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers, such as the Kozak sequence or Omega enhancer, and *Agrobacterium tumefaciens* nopalin synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic cells, such as transgenic plant cells, comprising the constructs of the present invention are provided, together with tissues and plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants.

In yet another aspect, methods for modulating the lignin, fructan or tannin content and composition of a target organism, such as a plant, are provided, such methods including stably incorporating into the genome of the target plant a genetic construct comprising a polynucleotide of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*. In a related aspect, a method for producing a plant having altered lignin, fructan or tannin

composition is provided, the method comprising transforming a plant cell with a genetic construct comprising of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of an enzyme in a target organism, such as a plant, comprising stably incorporating into the genome of the target organism a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

Brief Description of the Drawings

Fig. 1 shows the activity of recombinant LpSPP (SEQ ID NO: 8) and FaSPP (SEQ ID NO 7) on dephosphorylating Suc-6-P and Fru-6-P. The pET41a extract was the vector control.

Fig. 2 shows the peroxidase activity of PER3 (SEQ ID NO: 50) and PER5 (SEQ ID NO: 52) as determined by oxidation of ABTS. Horseradish peroxidase of known activity (Sigma, St Louis, MI) was used as a positive control and boiled samples as a negative control.

Fig. 3 shows PCR verification of transgenic *N. benthamiana* plants transformed with Lp6-SFT1 (SEQ ID NO: 3). Genomic DNA was isolated from kanamycin resistant T2 *N. benthamiana* plants and the Lp6-SFT fragment was amplified using specific PCR primers.

Fig. 4 shows PCR verification of transgenic *N. benthamiana* plants transformed with Lp1-SST (SEQ ID NO: 1). Genomic DNA was isolated from kanamycin resistant T2 *N. benthamiana* plants and the Lp1-SST fragment was amplified using specific PCR primers. Plant number 5 is a non-transgenic control.

Fig. 5 shows the fructan level in transgenic *N. benthamiana* lines transformed with Lp6-SFT1 (SEQ ID NO: 3) and Lp1-SST (SEQ ID NO: 1).

Fig. 6 shows the sucrose synthesizing activity of FaSPS-N (SEQ ID NO: 9) with and without SPP (SEQ ID NO: 8) in mammalian cell extracts. The non-transfected cells are controls.

Fig. 7 shows the sucrose cleaving activity of FaSUS1 (SEQ ID NO: 13) in mammalian cell extracts.

Fig. 8 shows the invertase activity for vacuolar invertase (SEQ ID NO: 25) and two cell wall invertases (SEQ ID NO: 17 and 19); absence of invertase activity from an empty vector (pPICZalphaA) control is also shown.

Detailed Description of the Invention

The polypeptides of the present invention, and the polynucleotides encoding the polypeptides, have activity in lignin, fructan and tannin biosynthetic pathways in plants. Using the methods and materials of the present invention, the lignin, fructan and/or tannin content of a plant may be modulated by modulating expression of polynucleotides of the present invention, or by modifying the polynucleotides or polypeptides encoded by polynucleotides. The isolated polynucleotides and polypeptides of the present invention may thus be usefully employed in the correction of nutritional imbalances associated with temperate pastures and to increase the yield of animal products from pastures.

The lignin, fructan and/or tannin content of a target organism, such as a plant, may be modified, for example, by incorporating additional copies of genes encoding enzymes involved in the lignin, fructan or tannin biosynthetic pathways into the genome of the target plant. Similarly, a modified lignin, fructan and/or tannin content can be obtained by transforming the target plant with anti-sense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the lignin, fructan and tannin biosynthetic pathways can be manipulated to modify the relative amount of each monomer unit synthesized, thereby leading to the formation of lignins, fructans or tannins having altered composition.

The present invention thus provides methods for modulating the polynucleotide and/or polypeptide content and composition of an organism, such methods involving stably incorporating into the genome of the organism a genetic construct comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant species, preferably a forage plant, more preferably a grass of the *Lolium* or *Festuca* species, and most preferably *Lolium perenne* or *Festuca arundinacea*. In related aspects, methods for producing a plant having an altered genotype or phenotype is provided, such methods

comprising transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth. Plants having an altered genotype or phenotype as a consequence of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such plants, and the progeny of such plants, are contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention have utility in genome mapping, in physical mapping, and in positional cloning of genes. Additionally, the polynucleotide sequences identified as SEQ ID NOS: 1-62 and 125-162 and their variants, may be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. Oligonucleotide probes designed using the polynucleotides of the present invention may be employed to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NO: 1-62 and 125-162, and polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 63-124 and 163-190. The polynucleotides and polypeptides of the present invention have demonstrated similarity to the following polypeptides that are known to be involved in lignin, fructan and tannin biosynthetic processes:

TABLE 1

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
1 and 125	63 and 163	Fructan biosynthesis	Homolog of Sucrose:Sucrose 1-fructosyl-transferase (1-SST) isolated from *Festuca arundinacea*. They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 120 to 133). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, *Biochem. J.* 280:309-316, 1991).
2	64	Fructan biosynthesis	Homolog of Sucrose:Sucrose 1-fructosyl-transferase (1-SST) isolated from *Festuca arundinacea*. It contains a typical signature of the glycosyl hydrolases family 32 (amino acid residues 120 to 133). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, *Biochem. J.* 280:309-316, 1991).
3 and 126	65 and 164	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from *Festuca arundinacea*. They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 90 to 564). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, *Biochem. J.* 280:309-316, 1991).
4 and 127	66 and 165	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from *Lolium perenne*. They contain a typical signature of the glycosyl hydrolases family 32 (amino acid residues 96 to 107). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, *Biochem. J.* 280:309-316, 1991).
5	67	Fructan biosynthesis	Homolog of sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from *Festuca arundinacea*.
6 and 128	68 and 166	Fructan biosynthesis	Homolog of Sucrose:fructan 6-fructosyl-transferase (6-SFT) isolated from *Lolium perenne*. They contain a typical signature of the glycosyl hydrolases family 32 (amino acid

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			residues 90 to 103). The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, *Biochem. J.* 280:309-316, 1991).
7 and 129	69	Fructan biosynthesis	Homolog of Sucrose-6-phosphate phospho-hydrolase (SPP; EC 3.1.3.24) isolated from *Festuca arundinacea*. This enzyme belongs to the superfamily of hydrolases, and has the three conserved motifs found in these proteins (Galperin and Koonin, *Trends Biochem Sci.* 23:127-129, 1998). Motif I (amino acid residues 10 to 19) contains conserved Asp and a Thr residues, motif II (amino acid residues 48 to 53) contains a conserved Thr residue, and Motif III (residues 167 to 220) contains conserved Lys (position 167) and Asp residues (position 202 and 206). These conserved amino acid residues are required for activity of the enzyme.
8	70	Fructan biosynthesis	Homolog of Sucrose-6-phosphate phospho-hydrolase (SPP; EC 3.1.3.24) isolated from *Lolium perenne*. This enzyme belongs to the superfamily of hydrolases, and has the three conserved motifs found in these proteins (Galperin and Koonin, *Trends Biochem Sci.* 23:127-129, 1998). Motif I (residues 10 to 19) contains conserved Asp and Thr residues, motif II (amino acid residues 48 to 53) contains a conserved Thr residue, and Motif III (amino acid residues 167 to 220) contains conserved Lys (position 167) and Asp residues (position 202 and 206). These conserved amino acid residues are required for activity of the enzyme.
9 and 130	71	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-1) isolated from *Festuca arundinacea*.
10 and 131	72 and 167	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-1) isolated from *Lolium perenne* and that is involved in the sucrose synthesis pathway.
11 and 132	73 and 168	Fructan biosynthesis	Homolog of sucrose phosphate synthase (SPS-N) isolated from *Lolium perenne* and that is involved in the sucrose synthesis pathway.
12 and 133	74 and 169	Fructan	Homolog of sucrose synthase (SuS) isolated

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
		biosynthesis	from *Lolium perenne*. These molecules contain a leucine zipper motif in amino acid position 191 to 213. Leucine zipper motifs are present in many gene regulatory proteins (Landschulz *et al.*, *Science* 240:1759-1764, 1988).
13	75	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from *Festuca arundinacea*. This molecule contains a leucine zipper motif in amino acid position 191 to 213. Leucine zipper motifs are present in many gene regulatory proteins (Landschulz *et al.*, *Science* 240:1759-1764, 1988).
14 and 134	76 and 170	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from *Lolium perenne*.
15	77	Fructan biosynthesis	Homolog of sucrose synthase (SuS) isolated from *Festuca arundinacea*.
16 and 135	78 and 171	Fructan biosynthesis	Homologue of cell wall invertase (CWINV) isolated from *Festuca arundinacea* that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved peptide domain in amino acid residues 139 to 144 and 242-247, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D (LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999).
17	79	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Lolium perenne* that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 70 to 74 and a peptide domain in amino acid residues 250 to 255. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acids 61 to 74 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, *J. Biol. Chem.* 265:10817-10120, 1990).
18 and 136	80 and 172	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Lolium perenne* that belongs to the family 32 of glycosyl hydrolases.
19	81	Fructan	Homolog of cell wall invertase (CWINV)

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
		biosynthesis	isolated from *Festuca arundinacea* that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 60 to 64. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acids 51 to 64 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, *J. Biol. Chem.* 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 24.
20 and 137	82 and 173	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Festuca arundinacea* that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 61 to 66and 242-247, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999).
21	83	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Festuca arundinacea* that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 73 to 77 and a peptide domain in amino acid residues 253 to 258. The consensus peptide domain of invertases is (WVYL)EC(PIL)D-(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 64 to 77 that contains a conserved His residue important in the catalytic reaction (Reddy and Maley, *J. Biol. Chem.* 265:10817-10120, 1990).
22 and 138	84 and 174	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Lolium perenne* that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 174 to 179 and 234 to 239,

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			respectively. The consensus peptide domain of invertases is (WVYL)EC- (PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999).
23	85	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Festuca arundinacea* that belongs to the family 32 of glycosyl hydrolases. This molecule contains a conserved pentapeptide bF-motif at amino acid residues 56 to 60. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 47 to 60 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, *J. Biol. Chem.* 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 22.
24 and 139	86 and 175	Fructan biosynthesis	Homolog of cell wall invertase (CWINV) isolated from *Lolium perenne* that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved pentapeptide bF-motif at amino acid residues 244 to 249. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999). They also contain a glycosyl hydrolases family 32 signature region at amino acid 56 to 69 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, *J. Biol. Chem.* 265:10817-10120, 1990). A signal peptide is present in amino acid residues 1 to 25.
25 and 140	87 and 176	Fructan biosynthesis	Homolog of vacuolar invertase (SINV) isolated from *Lolium perenne* that belongs to the family 32 of glycosyl hydrolases. These molecules contain a conserved pentapeptide bF-motif at amino acid residues 136 to 140 and 138 to 142, respectively and a peptide domain in amino acid residues 317 to 322 and 319 to 324, respectively. The consensus peptide domain of

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999). It also contains a glycosyl hydrolases family 32 signature region at amino acid 127 to 140 and 129 to 142 that contains a conserved His residue that is important in the catalytic reaction (Reddy and Maley, *J. Biol. Chem.* 265:10817-10120, 1990).
26 and 141	88 and 177	Fructan biosynthesis	Homolog of invertase (SINV) isolated from *Lolium perenne* that belongs to the family 32 of glycosyl hydrolases. These molecules contain a peptide domain in amino acid residues 143 to 148 and 184 to 189, respectively. The consensus peptide domain of invertases is (WVYL)EC(PIL)D(LFI) with the conserved Cys residue part of the catalytic domain (Sturm, *Plant Physiol.* 121:1-7, 1999).
27	89	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from *Lolium perenne* The molecule has two conserved AMP binding regions at amino acid residues 182 to 193 and 383 to 389 (Hu *et al.*, *Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray *et al.*, *Biochem. Mol. Biol. Int.* 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu *et al.*, *Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998).
28 and 142	90	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from *Lolium perenne*. The molecule has two conserved AMP binding regions at amino acid residues 195 to 206 and 395 to 401 (Hu *et al.*, *Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray *et al.*,

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			Biochem. Mol. Biol. Int. 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998).
29	91	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from *Festuca arundinacea*. The molecule has two conserved AMP binding regions at amino acid residues 195 to 206 and 395 to 401 (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray *et al., Biochem. Mol. Biol. Int.* 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998).
30 and 143	92 and 178	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from *Lolium*. The molecules have two conserved AMP binding regions at amino acid residues 194 to 205 and 394 to 400 (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray *et al., Biochem. Mol. Biol. Int.* 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998).
31	93	Lignin/Tannin biosynthesis	Homolog of 4-Coumarate:CoA ligase (4CL, EC 6.2.1.12) isolated from *Festuca*

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			arundinacea. The molecule has two conserved AMP binding regions at amino acid residues 194 to 206 and 482 to 490 (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998). The AMP-binding domain signature consists of two binding site motifs. The consensus of the first motif is LPYSSGTTGLPK (Etchegaray *et al., Biochem. Mol. Biol. Int.* 44:235-243, 1998). The region very rich in glycine, serine, and threonine followed by a conserved lysine. In most of these proteins, the residue that follows the Lys at the end of the pattern is a Gly. The second motif consensus sequence is GEIC(V/I)RG (Hu *et al., Proc. Natl. Acad. Sci. USA* 95:5407-5412, 1998).
32 and 144	94 and 179	Lignin/Tannin biosynthesis	Homolog of cinnamic acid 4-hydroxylase (C4H) isolated from *Lolium perenne*. The molecules have a conserved cytochrome P450 region in amino acids 436 to 445 that contains a conserved Cys residue involved in heme binding (Miles *et al., Biochim Biophys Acta* 1543:383-407, 2000).
33	95	Lignin/Tannin biosynthesis	Homolog of cinnamic acid 4-hydroxylase (C4H) isolated from Festuca arundinacea. The molecule has a conserved Cytochrome P450 region in amino acids 440 to 449 that contains a conserved Cys residue involved in heme binding. The cytochrome P450 cysteine heme-iron ligand signature consensus is FGxGRRSCPG where the conserved C is the heme iron ligand (Miles *et al., Biochim. Biophys. Acta* 1543:383-407, 2000). It also contains an aldehyde dehydrogenases active site (Hempel *et al., Adv. Exp. Med. Biol.* 436:53-59, 1999) at amino acid residues 428 to 435. A hydrophobic signal peptide region is present in amino acid residues 1 to 24.
34 and 145	96 and 180	Lignin biosynthesis	Homolog of cinnamyl-alcohol dehydrogenase (CAD; EC 1.1.1.195) isolated from *Lolium perenne*. These molecules contain a conserved zinc-containing alcohol dehydrogenase domain (Joernvall *et al., Eur. J. Biochem.* 167:195-201, 1987) in amino acid residues 69 to 83, with a conserved His residue at position 70. They also

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			contain a cytochrome C family heme-binding site signature (Mathews, *Prog. Biophys. Mol. Biol.* 45:1-56, 1985) in residues 45 to 50.
35	97	Lignin biosynthesis	Homolog of cinnamyl-alcohol dehydrogenase (CAD; EC 1.1.1.195) isolated from *Festuca arundinacea*. CAD belongs to the family of zinc-binding dehydrogenases. This molecule contains a conserved zinc-containing alcohol dehydrogenases domain (Joernvall *et al., Eur. J. Biochem.* 167:195-201, 1987) in amino acid residues 69 to 83, with a conserved His residue at position 70. It also contains a Cytochrome C family heme-binding site signature. The cytochrome C family heme-binding site signature is CGICHT. In the cytochrome C protein family, the heme group is covalently attached by thioether bonds to two conserved cysteine residues. The consensus sequence for this site is Cys-X-X-Cys-His and the histidine residue is one of the two axial ligands of the heme iron. This arrangement is shared by all proteins known to belong to cytochrome C family (Mathews, *Prog. Biophys. Mol. Biol.* 45:1-56, 1985).
36 and 146	98	Lignin biosynthesis	Homolog of caffeoyl coenzyme A O-methyltransferase (CCoAOMT) (EC 2.1.1.104) isolated from *Lolium perenne*.
37	99	Lignin biosynthesis	Homolog of caffeoyl coenzyme A O-methyltransferase (CCoAOMT) (EC 2.1.1.104) isolated from *Festuca arundinacea*.
38 and 147	100 and 181	Lignin biosynthesis	Homolog of cinnamoyl CoA:NADP oxidoreductase (CCR, EC 1.2.1.44) isolated from *Lolium perenne* that catalyzes the conversion of cinnamoyl CoA esters to their corresponding cinnamaldehydes in the first specific step in the synthesis of the lignin monomers. A hydrophobic region typical of a signal peptide is present in amino acid residues 1 to 24.
39 and 148	101	Lignin biosynthesis	Homolog of cinnamoyl CoA:NADP oxidoreductase (CCR, EC 1.2.1.44) isolated from *Festuca arundinacea* that catalyzes the conversion of cinnamoyl CoA esters to their corresponding cinnamaldehydes in the first

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			specific step in the synthesis of the lignin monomers.
40 and 149	102 and 182	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from *Festuca arundinacea* A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, *J. Biol. Chem.* 240:4727-4733, 1965).
41 and 150	103	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from *Lolium perenne* A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, *J. Biol. Chem.* 240:4727-4733, 1965).
42	104	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from *Festuca arundinacea* A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, *J. Biol. Chem.* 240:4727-4733, 1965).
43	105	Lignin biosynthesis	Homolog of caffeic acid 3-O-methyltransferase (COMT1) isolated from *Lolium perenne* A conserved consensus phosphopantetheine attachment site was identified in amino acid residues 47 to 62. This domain is involved in the attachment of activated fatty acid and amino-acid groups, with the Ser residue at position 52 crucial for the phosphopantetheine attachment (Pugh and Wakil, *J. Biol. Chem.* 240:4727-4733, 1965).
44 and 151	106 and 183	Lignin biosynthesis	Homolog of ferulate 5-hydroxylase (F5H) isolated from *Lolium perenne*. The molecules

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			have a conserved cytochrome P450 region in amino acids 463 to 472 that contains a conserved Cys residue involved in heme binding (Miles *et al.*, *Biochim Biophys Acta* 1543:383-407, 2000). A signal peptide is present in amino acid residues 1 to 30.
45	107	Lignin biosynthesis	Homolog of ferulate 5-hydroxylase (F5H) isolated from *Festuca arundinaceae*. The molecule has a conserved cytochrome P450 region in amino acids 462 to 471 that contains a conserved Cys residue involved in heme binding (Miles *et al.*, *Biochim Biophys Acta* 1543:383-407, 2000). A signal peptide is present in amino acid residues 1 to 30.
46 and 152	108	Lignin/Tannin biosynthesis	Homolog of phenylalanine ammonia-lyase (EC 4.3.1.5) (PAL) isolated from *Lolium perenne*. The polypeptide has a conserved PAL-histidase region in amino acid residues 193 to 209.
47 and 153	109 and 184	Lignin/Tannin biosynthesis	Homolog of phenylalanine ammonia-lyase (EC 4.3.1.5) (PAL) isolated from *Festuca arundinacea*. A conserved phenylalanine and histidine ammonia-lyases active site signature has been identified in amino acid residues 195 to 210.
48	110	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Festuca arundinacea*. The conserved peroxidase I region is present in amino acid residues 188 to 199 and contains a conserved His residue at position 196 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 60 to 71, with a conserved His residue at position 69 that is involved in heme binding (Kimura and Ikeda-Saito, *Proteins* 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 27.
49	111	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Lolium perenne*. The conserved peroxidase I region is present in amino acid residues 199 to 209 and contains a conserved His residue at position 208 in the active site. A signal peptide is present in amino acid residues 1 to 33.
50	112	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Festuca arundinacea*. The conserved

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			peroxidase I region is present in amino acid residues 180 to 190 and contains a conserved His residue at position 188 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 55 to 66, with a conserved His residue at position 64 that is involved in heme binding (Kimura and Ikeda-Saito, *Proteins* 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 22.
51 and 154	113	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Lolium perenne*. The conserved peroxidase I region is present in amino acid residues 199 to 209 and contains a conserved His residue at position 207 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 70 to 80, with a conserved His residue at position 78 that is involved in heme binding (Kimura and Ikeda-Saito, *Proteins* 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 20.
52 and 155	114	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Lolium perenne*. The conserved peroxidase I region is present in amino acid residues 198 to 208 and contains a conserved His residue at position 206 in the active site (Kimura and Ikeda-Saito, *Proteins* 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 34.
53, 156, and 162	115, 185, and 190	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Lolium perenne*. The conserved peroxidase I region is present in amino acid residues 157 to 168, 188 to 199, and 190 to 201, respectively and contain a conserved His residue at position 165, 196 and 198, respectively in the active site, and the conserved peroxidase 2 region is present in amino acid residues 29 to 41, 60 to 72 and 62 to 74, respectively, with a conserved His residue at position 38, 69 and 71, respectively that is involved in heme binding (Kimura and Ikeda-Saito, *Proteins* 3:113-120, 1988).
54	116	Lignin biosynthesis	Homolog of peroxidase (PER) isolated from *Festuca arundinacea*. The conserved

SEQ ID NO Polynucleotide	SEQ ID NO Polypeptide	Category	Description
			peroxidase I region is present in amino acid residues 176 to 186 and contains a conserved His residue at position 184 in the active site, and the conserved peroxidase 2 region is present in amino acid residues 55 to 67, with a conserved His residue at position 64 that is involved in heme binding (Kimura and Ikeda-Saito, *Proteins* 3:113-120, 1988). A signal peptide is present in amino acid residues 1 to 22.
55	117	Tannin Biosynthesis	Homolog of chalcone isomerase (CHI) isolated from *Lolium perenne*. The molecule contains a chalcone isomerase region at amino acid residues 1 to 213.
56	118	Tannin Biosynthesis	Homolog of chalcone isomerase (CHI). The molecule contains a chalcone isomerase region at amino acid residues 23 to 235.
57 and 157	119 and 186	Tannin Biosynthesis	Homolog of Chalcone Synthase (CHS) isolated from *Lolium perenne* and that is an important enzyme in flavonoid synthesis. The molecules contain a conserved chalcone synthase active site (Lanz *et al.*, *J. Biol. Chem.* 266:9971-9976, 1991) at amino acid residues 166 to 175, with the conserved Cys residue at position 167.
58 and 158	120 and 187	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from *Festuca arundinacea*.
59 and 159	121 and 188	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from *Lolium perenne*.
60 and 160	122 and 189	Tannin Biosynthesis	Homolog of dihydroflavonal-4-reductase (DFR) isolated from *Lolium perenne*. These molecules contain a conserved ATP/GTP binding site at amino acid residues 84 to 91 and 86 to 93, respectively, known as the "A" sequence (Walker *et al.*, *EMBO J.* 1:945-951, 1982) or "P-loop" (Saraste *et al.*, *Trends Biochem. Sci.* 15:430-434, 1990).
61 and 161	123	Tannin biosynthesis	Homolog of flavanone 3-βhydroxylase (F3βH) isolated from *Lolium perenne*.
62	124	Tannin Biosynthesis	Homolog of flavanone 3-βhydroxylase (F3βH) isolated from *Festuca arundinacea*.

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides, and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including RNAi, HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. A polynucleotide of the present invention may be an entire gene, or any portion thereof. As used herein, a "gene" is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20(8): 836-848, 1996.

In specific embodiments, the present invention provides isolated polynucleotides comprising a sequence of SEQ ID NO: 1-62 and 125-162; polynucleotides comprising variants of SEQ ID NO: 1-62 and 125-162; polynucleotides comprising extended sequences of SEQ ID NO: 1-62 and 125-162 and their variants, oligonucleotide primers and probes corresponding to the sequences set out in SEQ ID NO: 1-62 and 125-162 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of SEQ ID NO: 1-62 and 125-162 (*x*-mers), and polynucleotides comprising extended sequences which include portions of the sequences set out in SEQ ID NO: 1-62 and 125-162, all of which are referred to herein, collectively, as "polynucleotides of the present invention." Polynucleotides that comprise complements of such polynucleotide sequences, reverse complements of such polynucleotide sequences, or reverse sequences of such polynucleotide sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement(s)," "reverse complement(s)," and "reverse sequence(s)," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

Preferably, sequences that are complements of a specifically recited polynucleotide sequence are complementary over the entire length of the specific polynucleotide sequence.

As used herein, the term "*x*-mer," with reference to a specific value of "*x*," refers to a polynucleotide comprising at least a specified number ("*x*") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-62 and 125-162. The value of *x* may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polynucleotides identified as SEQ ID NO: 1-62 and 125-162, or their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polypeptides identified as SEQ ID NO: 63-124 and 163-190. According to preferred embodiments, the value of *x* is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NO: 1-62 and 125-162, or a variant of one of the polynucleotides corresponding to the polynucleotides provided in SEQ ID NO: 1-62 and 125-162. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 63-124 and 163-190, or a variant thereof.

Polynucleotides of the present invention were isolated by high throughput sequencing of cDNA libraries comprising forage grass tissue collected from *Lolium perenne* and *Festuca arundinacea*. Some of the polynucleotides of the present invention may be "partial" sequences, in that they do not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial

sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NO: 1-62 and 125-162 or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-62 and 125-162 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (x-mer) of one of the sequences of SEQ ID NOS: 1-62 and 125-162 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-62 and 125-162.

The polynucleotides identified as SEQ ID NOS: 1-62 and 125-162 contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides and functional portions of polypeptides. Additionally, open reading frames encoding polypeptides may be identified in extended or full length sequences corresponding to the sequences set out as SEQ ID NOS: 1-62 and 125-162. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are well known in the art and include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

The polynucleotides of the present invention may be isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue, as described below in Example 1. Alternatively, oligonucleotide probes and primers based on the sequences provided in SEQ ID NOS: 1-62 and 125-162 can be synthesized as detailed below, and used to identify positive clones in either cDNA or genomic DNA libraries from forage grass tissue cells by means of hybridization or polymerase chain reaction (PCR) techniques. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (*see*, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR technology*, Stockton Press: NY, 1989; and Sambrook *et al.*, eds., *Molecular cloning: a laboratory manual*, 2nd ed., CSHL Press: Cold Spring Harbor, NY, 1989). In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. Artificial analogs of DNA hybridizing specifically to target sequences could also be employed. Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

The polynucleotides of the present invention may also, or alternatively, be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (*e.g.*, Beckman Oligo 1000M DNA Synthesizer; Beckman Coulter Ltd., Fullerton, CA) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for

example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Oligonucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-62 and 125-162, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. An oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-62 and 125-162 or a variant thereof, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-62 and 125-162 or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions.

In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length, preferably from about 10 to 50 base pairs in length, and more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops, and other factors which are well known in the art. Preferred techniques for designing PCR primers are disclosed in Dieffenbach and Dyksler, *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program suitable for designing probes, and especially for

designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes.

The polynucleotides identified as SEQ ID NOS: 1-62 and 125-162 were isolated from cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-62 and 125-162.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a polynucleotide sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences.

In another aspect, the present invention provides isolated polypeptides encoded by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises a partial isolated polynucleotide sequence provided herein. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 63-124 and 163-190, as well as variants of such sequences.

As noted above, polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence of the present invention encoding the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and

higher eukaryotic cells. Preferably, the host cells employed are plant, *E. coli*, insect, yeast, or a mammalian cell line such as COS or293T. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof. The expressed polypeptides may be used in various assays known in the art to determine their biological activity. Such polypeptides may also be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 63-124 and 163-190, and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains an active site essential for affecting the function of the polypeptide, for example, a portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity. Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using methods well known to those of skill in the art, including the representative assays described below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may

be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably at least 90%, more preferably yet at least 95% and most preferably, at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotides and polypeptides having a specified percentage identity to a polynucleotide or polypeptide identified in one of SEQ ID NO: 1-190 thus share a high degree of similarity in their primary structure. In addition to a specified percentage identity to a polynucleotide or polypeptide of the present invention, variant polynucleotides and polypeptides preferably have additional structural and/or functional features in common with a polynucleotide of the present invention. Polynucleotides having a specified degree of identity to, or capable of hybridizing to, a polynucleotide of the present invention preferably additionally have at least one of the following features: (1) they contain an open reading frame, or partial open reading frame, encoding a polypeptide, or a functional portion of a polypeptide, having substantially the same functional properties as the polypeptide, or functional portion thereof, encoded by a polynucleotide in a recited SEQ ID NO:; or (2) they contain identifiable domains in common. Similarly, polypeptides having a specified degree of identity to a polypeptide of the present invention preferably additionally have at least one of the following features: (1) they have substantially the same functional properties as the polypeptide in the recited SEQ ID NO:; or (2) they contain identifiable domains in common.

Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides or amino acids in a specified region may be determined against another

polynucleotide or polypeptide, using computer algorithms that are publicly available. The BLASTN and FASTA algorithms, set to the default parameters described in the documentation and distributed with the algorithm, may be used for aligning and identifying the similarity of polynucleotide sequences. The alignment and similarity of polypeptide sequences may be examined using the BLASTP algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The FASTA and FASTX algorithms are described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and in Pearson, *Methods in Enzymol.* 183:63-98, 1990. The FASTA software package is available from the University of Virginia by contacting the Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The BLASTN software is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894. The BLASTN algorithm Version 2.0.11 [Jan-20-2000] and Version 2.2.1 [Apr-13-2001] set to the default parameters described in the documentation and distributed with the algorithm, are preferred for use in the determination of polynucleotide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res.* 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity for polynucleotides: Unix running command with the following default parameters: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq –o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the E values and percentage identity of

polypeptide sequences: blastall –p blastp –d swissprotdb –e 10 -G 0 -E 0 –v 30 –b 30 –i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA, or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23-nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The percentage identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion

of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleotides or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being related to the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being related to the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being related as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

In an alternative embodiment, variant polynucleotides are sequences that hybridize to a polynucleotide of the present invention under stringent conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as

probe composition, presence of organic solvents, and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. An example of "stringent conditions" is prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity to a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-62 and 125-162, or complements, reverse sequences, or reverse complements of those sequences, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-62 and 125-162, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 63-124 and 163-190 as a result of amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has activity in a lignin, fructan or tannin biosynthetic pathway.

In another aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or anti-sense direction. For applications where amplification of lignin, fructan or tannin synthesis is desired, the open reading frame may be inserted in the construct in a sense orientation, such that transformation of a target organism with the construct will lead to an increase in the number of copies of the gene and therefore an increase in the amount of enzyme. When down-regulation of lignin, fructan or tannin synthesis is desired, the open reading frame may be

inserted in the construct in an anti-sense orientation, such that the RNA produced by transcription of the polynucleotide is complementary to the endogenous mRNA sequence. This, in turn, will result in a decrease in the number of copies of the gene and therefore a decrease in the amount of enzyme. Alternatively, regulation may be achieved by inserting appropriate sequences or subsequences (*e.g.*, DNA or RNA) in ribozyme constructs.

Genetic constructs comprising a non-coding region of a gene coding for a polypeptide of the present invention, or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. As used herein the term "non-coding region" includes both transcribed sequences which are not translated, and non-transcribed sequences within about 2000 base pairs 5' or 3' of the translated sequences or open reading frames. Examples of non-coding regions which may be usefully employed in the inventive constructs include introns and 5'- non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of lignin, fructan or tannin synthesized by the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990; and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the gene. The gene promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist in introns (Luehrsen, *Mol. Gen. Genet.* 225:81-93, 1991). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For genetic constructs comprising either an open reading frame in an anti-sense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the genetic constructs of the present invention are well known in the art. The promoter gene sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the

promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are from the inventive sequences themselves.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter, will affect the activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or anti-sense RNA only in the tissue of interest. With DNA constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as *Lolium* or *Festuca*, are used. Grass promoters different from the original gene may also be usefully employed in the inventive genetic constructs in order to prevent feedback inhibition. For example, the fructosyltransferase gene will be regulated by sucrose sensing systems; therefore removing the gene from under control of its normal promoter allows the gene to be active all the time. Other examples of gene promoters which may be usefully employed in the present invention include, mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al.*, *Science* 244:174-181, 1989.

The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer

resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al.*, *in* Weissbach A and H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988). Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic construct of the present invention may be linked to a vector having at least one replication system, for example, *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of plants, both monocotyledonous (*e.g.*, grasses, maize/corn, grains, oats, rice, sorghum, millet, rye, sugar cane, wheat and barley), dicotyledonous (*e.g.*, *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and gymnosperms. In a preferred embodiment, the inventive genetic constructs are employed to transform grasses. Preferably the target plant is selected from the group consisting of *Lolium* and *Festuca* species, most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*. Other plants that may be usefully transformed with the inventive genetic constructs include other species of ryegrass and fescue, including, but not limited to *Lolium multiflorum* (Italian ryegrass), *Lolium hybridum* (hybrid ryegrass), *Lolium rigidum* (Wimerra grass), *Lolium temulentum* (darnel), *Festuca rubra* (red fescue) and *Festuca pratensis* (meadow fescue). As discussed above, transformation of a plant with a genetic construct of the present invention will produce a modified lignin, fructan or tannin content in the plant.

The production of RNA in target cells may be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target organism. A target plant may be transformed with more than one construct of the present invention, thereby modulating the lignin, fructan and/or tannin biosynthetic pathways by affecting the activity of more than one

enzyme, affecting enzyme activity in more than one tissue or affecting enzyme activity at more than one expression time. Similarly, a construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme. The polynucleotides of the present invention may also be employed in combination with other known sequences encoding enzymes involved in the lignin, fructan and/or tannin biosynthetic pathways. In this manner, more than one biosynthetic pathway may be modulated, or a lignin, fructan or tannin biosynthetic pathway may be added to a plant to produce a plant having an altered phenotype.

Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous plants and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res.* 12:8711-8721, 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic regions; cotyledons, hypocotyls, and the like. Transformation techniques which may be usefully employed in the inventive methods include those taught by Ellis *et al.*, *Plant Cell Reports*, 8:16-20, 1989; Wilson *et al.*, *Plant Cell Reports* 7:704-707, 1989; Tautorus *et al.*, *Theor. Appl. Genet.* 78:531-536, 198; Hiei *et al.*, *Plant J.* 6:271-282, 1994; and Ishida *et al.*, *Nature Biotechnol.* 14:745-750, 1996; US Patent 5,591,616; and European Patent Publication EP 672 752 A1. Once the cells are transformed, cells having the inventive DNA construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. The resulting transformed plants may be reproduced

sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

Polynucleotides of the present invention may also be used to specifically suppress gene expression by methods that operate post-transcriptionally to block the synthesis of products of targeted genes, such as RNA interference (RNAi), and quelling. For a review of techniques of gene suppression see *Science*, 288:1370-1372, 2000. Exemplary gene silencing methods are also provided in WO 99/49029 and WO 99/53050. Posttranscriptional gene silencing is brought about by a sequence-specific RNA degradation process which results in the rapid degradation of transcripts of sequence-related genes. Studies have provided evidence that double-stranded RNA may act as a mediator of sequence-specific gene silencing (see, e.g., review by Montgomery and Fire, *Trends in Genetics*, 14: 255-258, 1998). Gene constructs that produce transcripts with self-complementary regions are particularly efficient at gene silencing. A unique feature of this posttranscriptional gene silencing pathway is that silencing is not limited to the cells where it is initiated. The gene-silencing effects may be disseminated to other parts of an organism and even transmitted through the germ line to several generations.

The polynucleotides of the present invention may be employed to generate gene silencing constructs and or gene-specific self-complementary RNA sequences that can be delivered by conventional art-known methods to plant tissues, such as forage grass tissues. Within genetic constructs, sense and antisense sequences can be placed in regions flanking an intron sequence in proper splicing orientation with donor and acceptor splicing sites, such that intron sequences are removed during processing of the transcript and sense and antisense sequences, as well as splice junction sequences, bind together to form double-stranded RNA. Alternatively, spacer sequences of various lengths may be employed to separate self-complementary regions of sequence in the construct. During processing of the gene construct transcript, intron sequences are spliced-out, allowing sense and anti-sense sequences, as well as splice junction sequences, to bind forming double-stranded RNA. Select ribonucleases bind to and cleave the double-stranded RNA, thereby initiating the cascade of events leading to degradation of specific mRNA gene sequences, and silencing specific genes. Alternatively, rather than using a gene construct to express the self-complementary RNA sequences, the gene-specific double-stranded RNA segments are

delivered to one or more targeted areas to be internalized into the cell cytoplasm to exert a gene silencing effect. Gene silencing RNA sequences comprising the polynucleotides of the present invention are useful for creating genetically modified plants with desired phenotypes as well as for characterizing genes (e.g., in high-throughput screening of sequences), and studying their functions in intact organisms.

Example 1

ISOLATION OF cDNA SEQUENCES FROM *L. PERENNE* AND *F. ARUNDINACEA* cDNA LIBRARIES

L. perenne and *F. arundinacea* cDNA expression libraries were constructed and screened as follows. Tissue was collected from *L. perenne* and *F. arundinacea* during winter and spring, and snap-frozen in liquid nitrogen. The tissues collected include those obtained from leaf blades, leaf base, pseudostem, floral stems, inflorescences, roots and stem. Total RNA was isolated from each tissue type using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD). mRNA from each tissue type was obtained using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. cDNA expression libraries were constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene, La Jolla, CA), according to the manufacturer's protocol. The resulting cDNA clones were packaged using a Gigapack II Packaging Extract (Stratagene, La Jolla, CA) employing 1 μl of sample DNA from the 5 μl ligation mix. Mass excision of the libraries was done using XL1-Blue MRF' cells and XLOLR cells (Stratagene, La Jolla, CA) with ExAssist helper phage (Stratagene, La Jolla, CA). The excized phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing 5-bromo-4-chloro-3-indolyl-beta-D-galactosidase (X-gal) and isopropylthio-beta-galactoside (IPTG). Of the colonies plated and picked for DNA preparations, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and DNA was purified following standard protocols. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a

Biomek 2000 robot (Beckman Coulter Inc., Fullerton, CA) for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

The DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced from the 5' end. The polynucleotide sequences identified as SEQ ID NO: 4, 6, 11, 127, 128 and 132 were identified from *L. perenne* leaf cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 1, 14, 15, 26, 32, 36, 38, 41, 49, 125, 134, 141, 144, 147, and 150 were identified from *L. perenne* vegetative stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 17, 22, 25, 138, and 140 were identified from *L. perenne* leaf and pseudostem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 43, 57, 61, 157, and 161 were identified from *L. perenne* pseudostem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 10, 12, 28, 30, 34, 44, 60, 131, 133, 142, 143, 145, 151, and 160 were identified from *L. perenne* floral stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 8, 18, 46, 52, 53, 55, 59, 136, 152, 155, 156, 159, and 162 were identified from *L. perenne* stem cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 51 and 154 were identified from a *L. perenne* root cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 24, 27 and 139 were identified from *L. perenne* leaf blade cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 9, 37, 39, 40, 45, 130, 148, and 149 were identified from *F. arundinacea* basal leaf cDNA expression libraries; the polynucleotide sequences identified as SEQ ID NO: 19, 21, 29, 33, 35, 47, 48, and 153 were identified from *F. arundinacea* combined day 3 and day 6 basal leaves cDNA expression libraries; the polynucleotide sequence identified as SEQ ID NO: 54 was identified from a *F. arundinacea* combined day 3 and day 6 leaves cDNA expression library; the polynucleotide sequence identified as SEQ ID NO: 56 was identified from a *F. arundinacea* inflorescence cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 20 and 137 were identified from a subtracted *F. arundinacea* leaf blade cDNA expression library; the polynucleotide sequences identified as SEQ ID NO: 7, 23, 42, 50, 62, and 129 were identified from *F. arundinacea* pseudostem cDNA expression libraries; the polynucleotide

sequences identified as SEQ ID NO: 2, 13, 16 and 135 were identified from *F. arundinacea* leaf cDNA expression libraries; and the polynucleotide sequences identified as SEQ ID NO: 3, 5, 31, and 126 were identified from a *F. arundinacea* inflorescence day 0 cDNA expression library.

BLASTN Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the EMBL DNA database were made as of October 19, 2001 using BLASTN algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall –p blastn –d embldb –e 10 –G0 –E0 –r 1 –v 30 –b 30 –i queryseq –o. Comparisons of DNA sequences provided in SEQ ID NOS: 125-162 to sequences in the EMBL DNA database were made using BLASTN algorithm Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall –p blastn –d embldb -F F –e 10 –G0 –E0 –r 1 –v 2 –b 2 –i queryseq –o.

The sequences of SEQ ID NO: 4-6, 9-11, 17-19, 21-26, 33, 44, 45, 48, 49, 51-55, 59, 60, 130-132, 136, 139, 146, 151, 154-156, 159, and 162 were determined to have less than 50% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NO: 2, 3, 7, 8, 14, 16, 36-38, 46, 47, 50, 56-58, 61, 129, 135, 137, 138, 152, 153, 157, 158, 160 and 161 were determined to have less than 75% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 1, 12, 13, 15, 20, 28, 31, 32, 35, 40 62, 125-128, 133, 134, 142, 144 and 147 were determined to have less than 90% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequences of SEQ ID NOS: 29, 30, 39, 41-43, 141, 143, 148, and 149 were determined to have less than 98% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

BLASTP Polypeptide Analysis

The protein sequences corresponding to the isolated cDNA sequences were compared to sequences in the SwissProt/Trembl protein database using the computer algorithm

BLASTP. Comparisons of protein sequences provided in SEQ ID NOS: 63-124 to sequences in the SwissProt/Trembl protein database were made as of October 19, 2001 using BLASTP algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall –p blastp –dstdb–e 10 –G0 –E0 –v 30 –b 30 –i queryseq –o. Comparisons of protein sequences provided in SEQ ID NOS: 163-190 to sequences in the SwissProt/Trembl protein database were made using BLASTP algorithm Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall –p blastp –d stdb -F F –e 10 –G0 –E0 –v 2 –b 2 –i queryseq –o.

The sequences of SEQ ID NOS: 65-68, 72, 73, 78, 80, 81, 84, 85, 87, 88, 106, 107, 110,111, 113-115, 117, 118 and 121 were determined to have less than 50% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 71, 79, 82, 83, 86, 95, 98-100, 112, 116, 120, 122-124, 167, 168, 171-174, 185, 188, and 190 were determined to have less than 75% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 63, 64, 69, 70, 74-77, 90, 91, 93, 94, 97, 101, 102, 104, 108, 109, 119, 175, 183, 187, and 189 were determined to have less than 90% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NOS: 89, 92, 96, 103, 105, 163-165, 169, 170, 177, 179, 181, 184, and 186 were determined to have less than 98% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTP, as described above.

BLASTX Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the SwissProt/Trembl protein database using the computer algorithm BLASTX. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the SwissProt/Trembl protein database were made as of October 19, 2001 using BLASTX algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall –p blastx –dstdb –e 10 –G0 –E0 –v 30 –b 30 –i queryseq –o. Comparisons of DNA sequences provided in SEQ ID NOS: 1-62 to sequences in the SwissProt/Trembl protein database were made using BLASTX algorithm

Version 2.2.1 [Apr-13-2001], and the following Unix running command: blastall –p blastx –d stdb -F F –e 10 –G0 –E0 –v 2 –b 2 –i queryseq –o.

The sequences of SEQ ID NOS: 11, 44, 45, 48, 49, 51, 52, 55, 130, 132, 155, 156, and 162 were determined to have less than 50% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 3-10, 16-26, 33, 36-38, 40-43, 50, 53, 54, 56, 58-62, 129, 131, 135-139, 146, 150, 151, 154, and 158-161 were determined to have less than 75% identityto sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 1, 2, 12-15, 27, 28-32, 34, 35, 39, 46, 47, 57, 125-128, 133, 134, 141-145, 147-149, 152, 153, and 157 were determined to have less than 90% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above. Finally, the sequence of SEQ ID NO: 140 was determined to have less than 98% identity to sequences in the SwissProt/Trembl database using the computer algorithm BLASTX, as described above.

The location of open reading frames (ORFs), by nucleotide position, contained within the sequences of SEQ ID NO: 1-62 and 125-162, and the corresponding amino acid sequences are provided in Table 2 below. SEQ ID NO: 1-8, 10-15, 17, 19, 21, 23-25, 28-52, 54-59, 61-62 and 125-162 are believed to contain full-length ORFs.

TABLE 2

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
1	56-2,020	63
2	64-2,010	64
3	64-1,926	65
4	74-1,945	66
5	40-1,911	67
6	79-1,938	68
7	246-1,514	69
8	264-1,532	70
9	84-3,272	71
10	73-3,297	72
11	129-2,942	73
12	46-2,472	74
13	113-2,539	75
14	61-2,505	76

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
15	103-2,253	77
16	3-1,439	78
17	26-1,777	79
18	2-1,174	80
19	59-1,852	81
20	2-1,201	82
21	1-1,779	83
22	198-1,097	84
23	27-1,772	85
24	36-1,802	86
25	78-2,084	87
26	2-1,423	88
27	3-1,622	89
28	85-1,764	90
29	72-1,751	91
30	127-1,800	92
31	137-1,810	93
32	62-1,567	94
33	80-1,597	95
34	32-1,117	96
35	86-1,171	97
36	55-852	98
37	75-872	99
38	149-1,240	100
39	90-1,118	101
40	28-1,110	102
41	66-1,148	103
42	64-1,146	104
43	85-1,170	105
44	88-1,683	106
45	93-1,721	107
46	111-2,246	108
47	144-2,285	109
48	22-993	110
49	4-1,038	111
50	87-1,067	112
51	59-1,135	113
52	18-1,052	114
53	1-882	115
54	80-1,015	116
55	322-1,014	117
56	172-762	118
57	118-1,299	119

POLYNUCLEOTIDE SEQ ID NO:	ORF	POLYPEPTIDE SEQ ID NO:
58	5-595	120
59	14-1,003	121
60	1-987	122
61	65-1,174	123
62	103-1,245	124
125	55-2,019	163
126	63-1,925	164
127	73-1,944	165
128	71-1,930	166
131	72-3,299	167
132	134-2,950	168
133	45-2,471	169
134	65-2,512	170
135	74-1,819	171
136	170-1,855	172
137	28-1,770	173
138	26-1,733	174
139	35-1,801	175
140	71-2,083	176
141	63-1,607	177
143	126-1,799	178
144	61-1,566	179
145	67-1,152	180
147	148-1,239	181
149	27-1,109	182
151	87-1,718	183
153	143-2,284	184
156	46-1,017	185
157	117-1,313	186
158	81-1,193	187
159	12-1,001	188
160	26-1,018	189
162	50-1,027	190

SEQ ID NO: 125 and 163 are related to SEQ ID NO: 1 and 63, respectively; SEQ ID NO: 126 and 164 are related to SEQ ID NO: 3 and 65, respectively; SEQ ID NO: 127 and 165 are related to SEQ ID NO: 4 and 66, respectively; SEQ ID NO: 128 and 166 are related to SEQ ID NO: 6 and 68, respectively; SEQ ID NO: 129 is an extended sequence of SEQ ID NO: 7; SEQ ID NO: 130 is an extended sequence of SEQ ID NO: 9; SEQ ID NO: 131 and 167 are related to SEQ ID NO: 10 and 72, respectively; SEQ ID NO: 132 and 168 are related

to SEQ ID NO: 11 and 73, respectively; SEQ ID NO: 133 and 169 are related to SEQ ID NO: 12 and 74, respectively; SEQ ID NO: 134 and 170 are related to SEQ ID NO: 14 and 76, respectively; SEQ ID NO: 135 and 171 are full-length sequences of SEQ ID NO: 16 and 78, respectively; SEQ ID NO: 136 and 172 are full-length sequences of SEQ ID NO: 18 and 80, respectively; SEQ ID NO: 137 and 173 are related to SEQ ID NO: 20 and 82, respectively; SEQ ID NO: 138 and 174 are full-length sequences of SEQ ID NO: 22 and 84, respectively; SEQ ID NO: 139 and 175 are related to SEQ ID NO: 24 and 86, respectively; SEQ ID NO: 140 and 176 are related to SEQ ID NO: 25 and 87, respectively; SEQ ID NO: 141 and 177 are full-length sequences of SEQ ID NO: 26 and 88, respectively; SEQ ID NO: 142 is related to SEQ ID NO: 28 and encodes the same amino acid sequence; SEQ ID NO: 143 and 178 are related to SEQ ID NO: 30 and 92, respectively; SEQ ID NO: 144 and 179 are related to SEQ ID NO: 32 and 94, respectively; SEQ ID NO: 145 and 180 are full-length sequences of SEQ ID NO: 34 and 96, respectively; SEQ ID NO: 146 is related to SEQ ID NO: 36 and encodes the same amino acid sequence; SEQ ID NO: 147 and 181 are related to SEQ ID NO: 38 and 100, respectively; SEQ ID NO: 148 is related to SEQ ID NO: 39, and encodes the same amino acid sequence; SEQ ID NO: 149 and 182 are related to SEQ ID NO: 40 and 102, respectively; SEQ ID NO: 150 is related to SEQ ID NO: 41 and encodes the same amino acid sequence; SEQ ID NO: 151 and 183 is related to SEQ ID NO: 44 and 106, respectively; SEQ ID NO: 152 is related to SEQ ID NO: 46, and encodes the same amino acid sequence; SEQ ID NO: 153 and 184 are related to SEQ ID NO: 47 and 109, respectively; SEQ ID NO: 154 is related to SEQ ID NO: 51, and encodes the same amino acid sequence; SEQ ID NO: 155 is related to SEQ ID NO: 52, and encodes the same amino acid sequence; SEQ ID NO: 156 and 185 are full-length sequences of SEQ ID NO: 53 and 115, respectively; SEQ ID NO: 162 and 190 are variants of SEQ ID NO: 156 and 185, respectively, with a difference in the 5' region of SEQ ID NO: 156 and 162; SEQ NO: 157 and 186 are related to SEQ ID NO: 57 and 119, respectively; SEQ ID NO: 158 and 187 are related to SEQ ID NO: 58 and 120, respectively; SEQ ID NO: 159 and 188 are full-length sequences of SEQ ID NO: 59 and 121, respectively; SEQ ID NO: 160 and 189 are full-length sequences of SEQ ID NO: 60 and 122, respectively; and SEQ ID NO: 161 is related to SEQ ID NO: 61 and encodes the same amino acid sequence.

Example 2

USE OF SUCROSE PHOSPHATE PHOSPHATASE TO DEPHOSPHORYLATE SUCROSE-6-PHOSPHATE

The *F. arundinacea* and *L. perenne* FaSPP and LpSPP genes (SEQ ID NO: 7 and 8, respectively) share amino acid sequence identity with sucrose-6-phosphate phosphatase genes from other plant species (Lunn *et al., Proc. Natl. Acad. Sci. USA* 97:12914-12919, 2000). These genes were amplified by PCR using the primers given in SEQ ID NO: 191 and 192 to add an initiating methionine, and then cloned into the pET41a expression plasmid. These primers amplified nucleotides 263-1531 and 280-1548 for FaSPP and LpSPP, respectively. The resulting plasmids were transformed into *E. coli* BL21 cells using standard protocols, and protein expression was induced using IPTG.

The soluble recombinant protein was assayed for its ability to specifically dephosphorylate sucrose-6-phosphate (Suc-6-P) but not fructose-6-phosphate (Fru-6-P) using the procedure described by Lunn *et al.* (*ibid.*). The release of phosphate from Suc-6P and Fru-6-P was measured using the Fiske-Subbarow method of determining inorganic phosphate (SIGMA assay kit; Sigma, St Louis, MI), with the change in absorbance at 660 nm being proportional to the amount of phosphate released per unit time. As shown in Fig. 1, both the *Festuca* and *Lolium* SPP enzymes dephosphorylated Suc-6-P but not Fru-6-P, whereas control pET41 extract had no activity on either substrate.

Example 3

PEROXIDASE ACTIVITY OF GRASS ENZYMES DEMONSTRATED BY THEIR ABILITY TO OXIDIZE 2,2'AZINO-BIS.3-ETHYLBENZYLTHIAZOLINE-6-SULFONIC ACID (ABTS)

A number of *L. perenne* or *F. arundinacea* genes (SEQ ID NO: 48 – 54) share amino acid identity with peroxidase genes from other plant species (Hiraga *et al., Plant Cell Physiol.* 42:462-468, 2001). The putative amino acid secretion signal sequence was identified by signalP analysis of the *Lolium* and *Festuca* sequences and homology to known peroxidase proteins. Primers were designed to amplify DNA representing the mature protein (minus signal sequence; Table 3.). These genes were amplified by PCR to add an initiating methionine and then cloned into the pET25b expression plasmid. The resulting plasmid was

transformed into *E. coli* AD494 (DE3) pLysS cells using standard protocols, and protein expression was induced using IPTG.

TABLE 3

SEQ ID NO DNA	SEQ ID NO PROT	Gene	Primers SEQ ID NO:	DNA bp amplified	Protein codons
50	112	FaPER3	193 194	156-1077	24-326
52	114	LpPER5	195 196	120-1052	35-344

The insoluble recombinant protein was solubilized and re-folded following protocols described for several recombinant *Arabidopsis* peroxidases (Teilum *et al., Protein Exp. and Purif.* 15:77-82, 1999). The insoluble inclusion bodies within *E. coli* were isolated from lysed cells by standard protocols and the recombinant protein solubilized in 8M urea. The solubilized peroxidase protein was refolded to gain active enzyme by diluting urea to 2M with 5μM Heme, 0.25mM Glutathione reduced, and 0.45mM Glutathione oxidized, pH 8 (20mM Tris-HCl). The refolded protein was used directly to assay peroxidase activity.

Peroxidase activity was measured by incubating recombinant peroxidase with pre-mixed ABTS/H_2O_2 liquid substrate (Sigma, St Louis, MI) and measuring ABTS oxidation by the increase in absorbance at 405nm. Horseradish peroxidase of known activity (Sigma, St Louis, MI) was used as a positive control and boiled samples as a negative control. The results provided in Fig. 2 show that FaPER3 and LpPER5 (SEQ ID NO: 50 and 52, respectively) had similar activity to that of horseradish peroxidase in these assays.

Example 4

USE OF GRASS FRUCTOSYLTRANSFERASE GENES TO SYNTHESIZE FRUCTANS

Transformation of *N. benthamiana* plants with fructosyltransferase genes

Sense constructs containing a polynucleotide including the coding region of fructosyltransferase genes isolated from *L. perenne* Lp1-SST and Lp6SFT1 (SEQ ID NO: 125 and 126, respectively) were inserted into a pART27 derived binary vector and used to

transform *A. tumefaciens* LBA4404 using published methods (*see*, An *et al.*, "Binary Vectors," *in* Gelvin and Schilperoort, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR). The primers px17 (SEQ ID NO: 207) and px18 (SEQ ID NO: 208) were used to confirm the presence of the Lp1-SST construct, whereas the primers px19 (SEQ ID NO: 209) and px 20 (SEQ ID NO: 210) were used to confirm the presence of the Lp6-SFT-1 construct.

The *A. tumefaciens* containing the sense gene constructs were used to transform *N. benthamiana* leaf discs (Burow *et al.*, *Plant Mol. Biol. Report* 8:124-139, 1990). Several independent transformed plant lines were established for the sense construct for each fructosyltransferase gene. DNA was isolated from transformed plants containing the appropriate fructosyltransferase gene construct using the QIAGEN DNAeasy Plant Mini Kit (Qiagen, Valencia, CA). Presence of the fructosyltransferase gene was verified using PCR experiments as shown in Figs. 3 and 4. For the Lp6-SFT1 gene, the forward and reverse primers given in SEQ ID NO: 197 and 198 were used, respectively. These primers amplify nucleotides 1572 - 1980 of the Lp6-SFT1 gene which corresponds to a 406 base pair fragment. For Lp1-SST, the forward and reverse primers given in SEQ ID NO: 199 and 200 were used, respectively. These primers amplify nucleotides 1332 - 1740 of Lp1-SST, corresponding to a 414 base pair fragment.

<u>Effects of fructosyltransferase genes on fructosyltransferase concentration in transformed plants</u>

Fructans are not normally found in *N. benthamiana* plants; hence, if introduction of the sense fructosyltransferase constructs was successful, it should be possible to extract fructans from the transformed plants. The concentration of fructosyltransferase in the transformed plants was determined using the Fructan Assay Kit (Megazyme International Ireland Ltd, Wicklow, Ireland). Briefly, 300 mg of leaf material from the independent transformed plant lines containing the fructosyltransferase sense constructs were extracted individually at 80 °C with 1 ml 80% ethanol, followed by two 1 ml extractions with water. The ethanol and water extracts were combined and frozen overnight at – 20 °C. Extracts were centrifuged at 20,000 *g* to pellet chlorophyll. Clarified extracts were treated with 1%

PVP-40 to precipitate phenolic compounds. These extracts were then reduced in volume by rotary evaporation.

Fructan levels were determined in these extracts using the Megazyme Fructan Assay kit. Briefly, sucrose, starch and reducing sugars are removed from the plant carbohydrate extracts by using sucrase, β-amylase, pullulanase and maltase, and then converting the resulting reducing sugars to sugar alcohols. The remaining fructans are hydrolyzed with fructanase and the reducing sugars produced (glucose and fructose) are measured by the 4-hydroxybenzoic acid hydrazide (PAHBAH) reducing sugar method. The final extracts are assayed for absorbance at 410 nm. As shown in Fig. 5, fructans could be detected in both the Lp1-SST and Lp6-SFT-1 transgenic lines. Fructan levels were highest in lines 07, 09 and 12 for Lp1-SST, and lines 05 and 12 for Lp6SFT-1.

Example 5

USE OF SUCROSE PHOSPHATE SYNTHASE ENZYMES TO SYNTHESIZE SUCROSE

A *F. arundinacea* gene (FaSPS-N; SEQ ID NO: 9) has been identified that shares amino acid sequence identity with sucrose phosphate synthase (SPS) from other plant species. SEQ ID NO: 7 and 8 are also SPS sequences, with SEQ ID NO: 7 being a *Lolium perenne* homologue of SEQ ID NO: 9. The FaSPS-N was cloned into the pcDNA3 mammalian expression plasmid and the resulting plasmid transfected into 293T mammalian cells (human embryonic kidney derived cells) using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA).

Cell lysates from transfected cells were deionized on G25 spin columns and used in a sucrose synthesis assay. In this assay, mammalian cell extracts were tested for their ability to synthesize sucrose from fructose-6-phosphate and uridine 5'-diphosphoglucose. Following the synthesis reaction, hexoses were converted to sugar alcohols by boiling in the presence of 30% KOH. The sucrose synthesized was detected by the addition of 1.4 % anthrone reagent in H_2SO_4 and incubating at 40 °C for 20 min. The change in absorbance at 620 nm is relative to sucrose in the reaction (Botha and Black, *Aust. J. Plant Physiol.* 27:81-85, 2000). In these experiments, introducing FaSPS-N alone into mammalian cells produced a sucrose synthesis activity that was not detected in non-transfected cells (Fig. 6).

A known cofactor for SPS is SPP. To test whether SPP is required for SPS activity, the *L. perenne* LpSPP gene (SEQ ID NO: 8) was cloned into the pcDNA3 mammalian expression plasmid. Both the FaSPS-N and LpSPP plasmids were co-transfected into 293T mammalian cells using Lipofectamine 2000 reagent (Invitrogen, Carlsbad, CA). Cell lysates from transfected cells were deionized on G25 spin columns and used in a sucrose synthesis assay as described above. As shown in Fig. 6, adding SPP did not significantly enhance or alter the sucrose synthesis activity of the cell extracts.

Example 6

USE OF SOLUBLE SUCROSE SYNTHASE ENZYMES TO CLEAVE SUCROSE

A *F. arundinacea* gene (FaSUS-1; SEQ ID NO: 13) was identified that shared amino acid sequence identity with soluble sucrose synthase enzymes (SUS) from other plant species. The FaSUS-1 gene was cloned into the pcDNA3 mammalian expression plasmid, which was transiently transfected into 293T mammalian cells (human embryonic kidney derived cells) using Lipofectamine 2000 reagent (Invitrogen Carlsbad, CA). Transfected cells were grown for several days before harvesting (by scraping cells in a sucrose synthase buffer). Harvested cells were frozen on dry ice and freeze-thawed twice before pelleting cell debris by centrifugation. The resulting supernatant (cell lysate) was deionized on G25 spin columns and then used in a sucrose cleavage assay as described by Sebkova *et al.* (*Plant Physiol.* 108:75-83, 1995). In these assays, the cell lysates were tested for their ability to cleave sucrose in the presence of UDP to produce fructose and uridine 5'-diphosphoglucose. Following a 30 min incubation at 30 °C, the enzyme activity was stopped by boiling the tubes for 1 min. Both NAD and UDP-glucose dehydrogenase were added and the change in OD at 340 nM (production of NADPH) was measured. As shown in Fig. 7, significantly higher levels of sucrose cleavage were observed in cells transfected with FaSUS1 construct than in non-transfected control cells.

Example 7

USE OF ACID INVERTASES TO CLEAVE SUCROSE

A number of acid (vacuolar and cell wall) invertase genes from *L. perenne* and *F. arundinacea* (SEQ ID NOS: 17, 19, 21, 23 and 135-141) were identified that share amino acid sequence identity with acid invertases from other plant species (Unger *et al., Plant Physiol.* 104:1351-1357, 1994; Goetz and Roitsch, *J. Plant Physiol.* 157:581-585, 2000). These sequences were analysed by SignalP and homology to identify signal regions and propeptide sequences, and primers were designed to amplify the DNA sequence encoding the mature protein (Table 4).

TABLE 4

SEQ ID NO DNA	SEQ ID NO PROT	Gene	Primers SEQ ID NO	DNA bp amplified	Protein codons
17	79	LpCWINV1	201 202	137-1803	38-583
19	81	FaCWINV4	203 204	134-1912	26-597
25	87	LpSINV1	205 206	387-2124	104-668

The PCR fragments were cloned into pPICZαA vectors for expression in methylotrophic yeast *Pichia pastoris* (EasySelect TM Pichia Expression Kit, Invitrogen, Carlsbad, CA). The sequences were cloned in frame with the α-mating factor for secretion of the recombinant invertase protein into liquid media, following similar methods described for the expression of barley 6-SFT and fescue 1-SST in *P. pastoris* (Hochstrasser *et al., FEBS Letters* 440:356-360, 1998; Lüscher *et al., Plant Physiol.*, 124:1217-1227, 2000). The media was concentrated 10 fold by Vivaspin 30 kDa spin column (VivaScience, Hannover, Germany) to concentrate recombinant protein and used directly to assay invertase activity. Recombinant protein was assayed with 100mM sucrose in 500 μl phosphate buffer pH5.0, at 30 °C for 1 hour. Release of glucose by invertase activity was measured using a glucose HK assay kit (Sigma, St Louis, MI). Fig. 8 shows the glucose released by invertase activity in terms of glucose concentration in the assay mix. As shown in Fig. 8, invertase activity was observed for the vacuolar invertase (LpSINV1; SEQ NO: 25) and the two cell wall invertases

(LpCWINV1 and FaCWINV4; SEQ NO: 17 and 19, respectively) but not for an empty vector (pPICZalphaA) control.

Example 8

USE OF TANNIN GENES TO MODIFY TANNIN BIOSYNTHESIS

Certain *Arabidopsis* mutants of the *transparent testa* (*tt*) phenotype do not make the anthocyanin pigment cyanidin and therefore have no seed coat color. The genes responsible for many of these mutants have now been identified as shown in Table 5.

TABLE 5

Enzyme	Abbreviation	Locus	Chromosome
Dihydroflavanol-4-reductase	DFR	*tt3*	5
Chalcone synthase	CHS	*tt4*	5
Chalcone isomerase	CHI	*tt5*	3
Flavanone 3- β-hydroxylase	F3βH	*tt6*	3

Over-expression of the maize genes for CHS, CHI and DFR has been shown to complement the *Arabidopsis tt4, tt5* and *tt3* mutants, respectively, thereby restoring cyanidin synthesis and seed coat color (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Complementation of these *Arabidopsis* mutants may therefore be employed to demonstrate the function of the inventive polynucleotides encoding enzymes involved in the tannin biosynthetic pathway.

Sense constructs containing a polynucleotide including the coding region of tannin genes isolated from *L. perenne* or *F. arundinacea* LpCHS, LpCHI, LpF3βH, LpDFR1, FaCHI and FaF3βH (SEQ ID NO: 157, 55, 161, 159, 56 and 62, respectively) under the control of the CaMV 35S promoter were inserted into a binary vector and used to transform *Agrobacterium tumefaciens* LBA4404 using published methods (*see*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," *in* Gelvin SB, Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR) using the primer pairs described in Table 6.

TABLE 6

Gene	SEQ ID NO:	Transparent testa line	Forward Primer SEQ ID NO:	Reverse Primer SEQ ID NO:
LpCHS	157	*tt4*	211	212
LpCHI	55	*tt5*	213	214
LpF3βH	161	*tt6*	217	218
LpDFR1	159	*tt3*	215	216
FaCHI	56	*tt5*	213	214
FaF3βH	62	*tt6*	217	218

The *A. tumefaciens* containing the sense gene constructs are used to transform *Arabidopsis* by floral dipping (Clough and Bent, *Plant J.* 16:735-743, 1998). Several independent transformed plant lines were established for the sense construct for each of the tannin genes. Specifically, LpDFR1 constructs were transformed into *Arabidopsis tt3* mutants, LpCHS constructs were transformed into *Arabidopsis tt4* mutants, LpCHI and FaCHI constructs were transformed into *Arabidopsis tt5* mutants, and LpF3βH and FaF3βH constructs were transformed into *Arabidopsis tt6* mutants. Several independent transformed plant lines were established for the construct for each of the tannin genes. Transformed plants containing the appropriate tannin gene construct were verified using PCR.

The presence of cyanidin in the FaCHI transformed plants is demonstrated by a phenotypic change in plant seedling color and by analyzing cyanidin extracts made from transgenic plants grown under stressed conditions (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Briefly, cyanidins are extracted from plant tissue with an acid/alcohol solution (HCl/methanol) and water. Chlorophyll is removed by freezing the extracts followed by centrifugation at 4 °C at 20,000 *g* for 20 min. Any remaining chlorophyll is removed through a chloroform extraction. The absorbance at 530 nm is measured for each of the cyanidin extracts. Non-transgenic wild type and control *Arabidopsis* plants are used as controls.

SEQ ID NOS: 1-218 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

Claims

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

   (a) SEQ ID NO: 1-62 and 125-162;

   (b) complements of SEQ ID NO: 1-62 and 125-162;

   (c) reverse complements of SEQ ID NO: 1-62 and 125-162; and

   (d) reverse sequences of SEQ ID NO: 1-62 and 125-162;

2. An isolated polynucleotide comprising a sequence selected from the group consisting of:

   (a) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of SEQ ID NO: 1-62 and 125-162;

   (b) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-62 and 125-162;

   (c) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-62 and 125-162; and

   (d) sequences having at least 95% identity to a sequence of SEQ ID NO: 1-62 and 125-162,

wherein the polynucleotide encodes a polypeptide having substantially the same functional properties as a polypeptide encoded by SEQ ID NO: 1-62 and 125-162.

3. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.

4. A kit comprising a plurality of oligonucleotide probes or primers of claim 3.

5. A genetic construct comprising an isolated polynucleotide of any one of claims 1 and 2.

6. A transgenic cell comprising a construct according to claim 5.

7. A construct comprising, in the 5'-3' direction:
   (a) a gene promoter sequence;
   (b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide encoded by a polynucleotide of any one of claims 1 and 2; and (2) a polynucleotide comprising a non-coding region of a polynucleotide of any one of claims 1 and 2; and
   (c) a gene termination sequence.

8. The construct of claim 7, wherein the polynucleotide is in a sense orientation.

9. The construct of claim 7, wherein the polynucleotide is in an anti-sense orientation.

10. A transgenic plant cell comprising a construct of claim 7.

11. A plant comprising a transgenic plant cell according to claim 10, or fruit or seeds or progeny thereof.

12. A method for modulating one or more of the lignin composition, fructan composition and tannin composition of a plant, comprising stably incorporating into the genome of the plant at least one polynucleotide of any one of claims 1 and 2.

13. The method of claim 12, wherein the plant is selected from the group consisting of grasses.

14. The method of claim 13, wherein the plant is selected from the group consisting of: *Lolium perenne* and *Festuca arundinacea*.

15. The method of claim 12 comprising stably incorporating into the genome of the plant a construct of claim 7.

16. A method for producing a plant having one or more of altered lignin composition, altered fructan composition and altered tannin composition, comprising:

(a) transforming a plant cell with a construct of claim 7 to provide a transgenic cell; and

(b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

17. A method for modifying the activity of a polypeptide involved in a lignin, fructan or tannin biosynthetic pathway in a plant comprising stably incorporating into the genome of the plant a construct of claim 7.

18. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 63-124 and 163-190.

19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences having at least 75% identity to a sequence of SEQ ID NO: 63-124 and 163-190;

(b) sequences having at least 90% identity to a sequence of SEQ ID NO: 63-124 and 163-190; and

(c) sequences having at least 95% identity to a sequence of SEQ ID NO: 63-124 and 163-190

wherein the polypeptide has substantially the same functional properties as a polypeptide of SEQ ID NO: 63-124 and 163-190.

20. An isolated polynucleotide that encodes a polypeptide of claim 18.

21. An isolated polypeptide encoded by a polynucleotide of any one of claims 1 and 2.

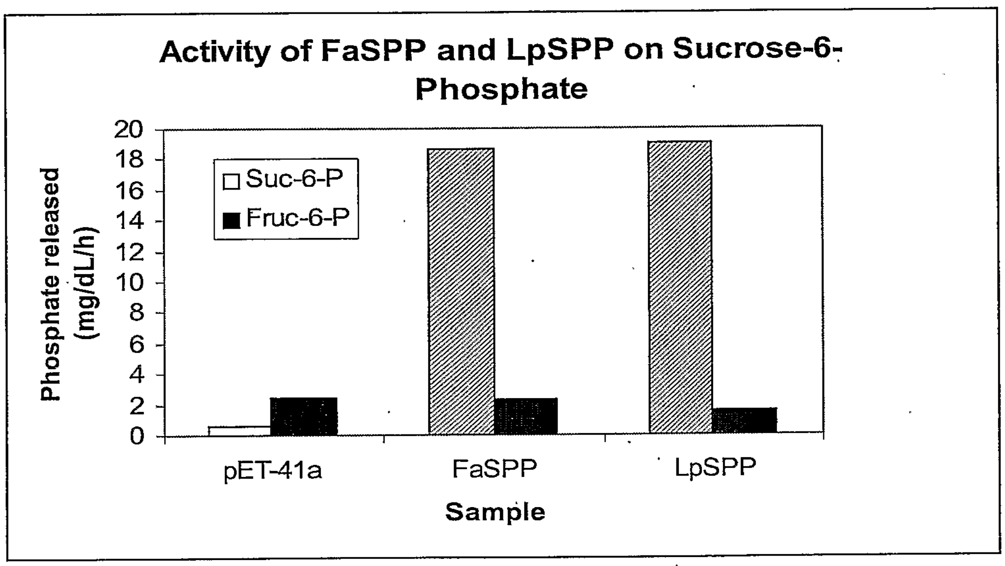

Activity of FaSPP and LpSPP on Sucrose-6-Phosphate
Phosphate released (mg/dL/h)
20
18
16
14
12
10
8
6
4
2
0
Suc-6-P
Fruc-6-P
pET-41a
FaSPP
LpSPP
Sample

Figure 1.

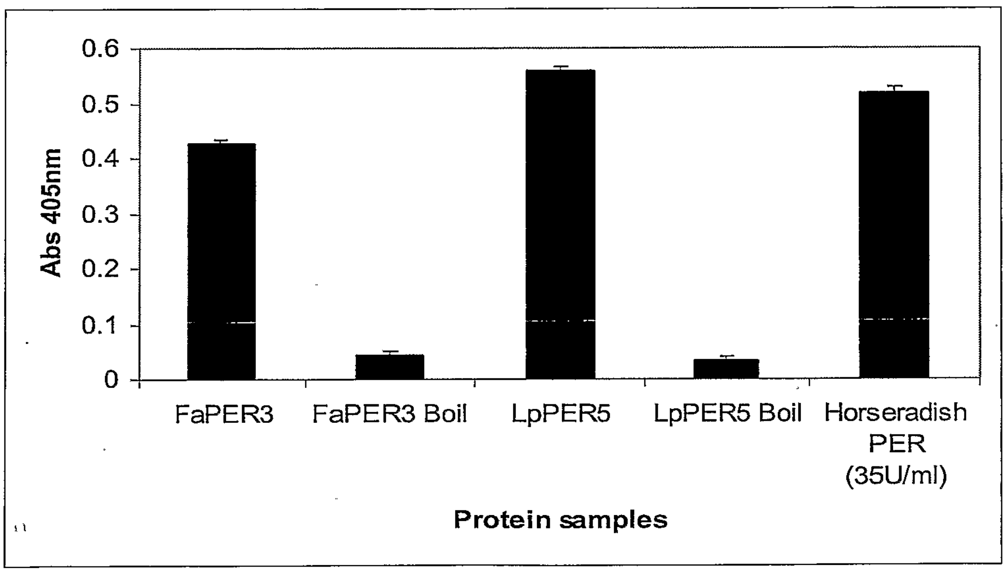
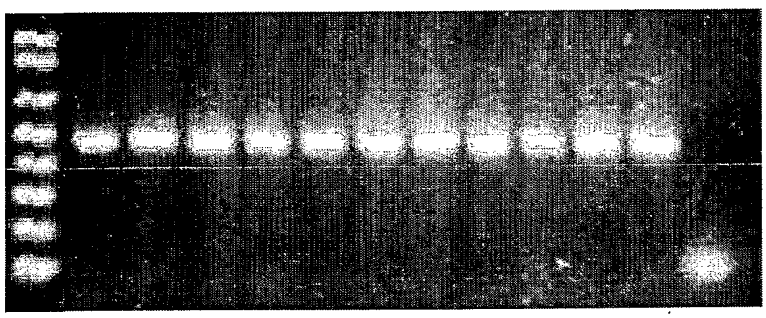

0.6
0.5
0.4
0.3
0.2
0.1
0
Abs 405nm
FaPER3
FaPER3 Boil
LpPER5
LpPER5 Boil
Horseradish PER (35U/ml)
Protein samples

Figure 2.

M 1 2 3 4 5 6 7 9 11 12 C



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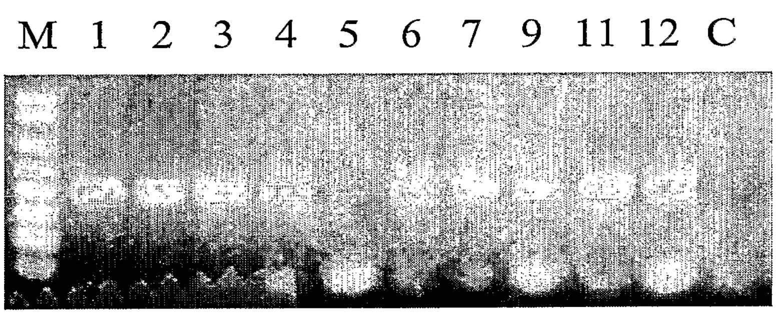

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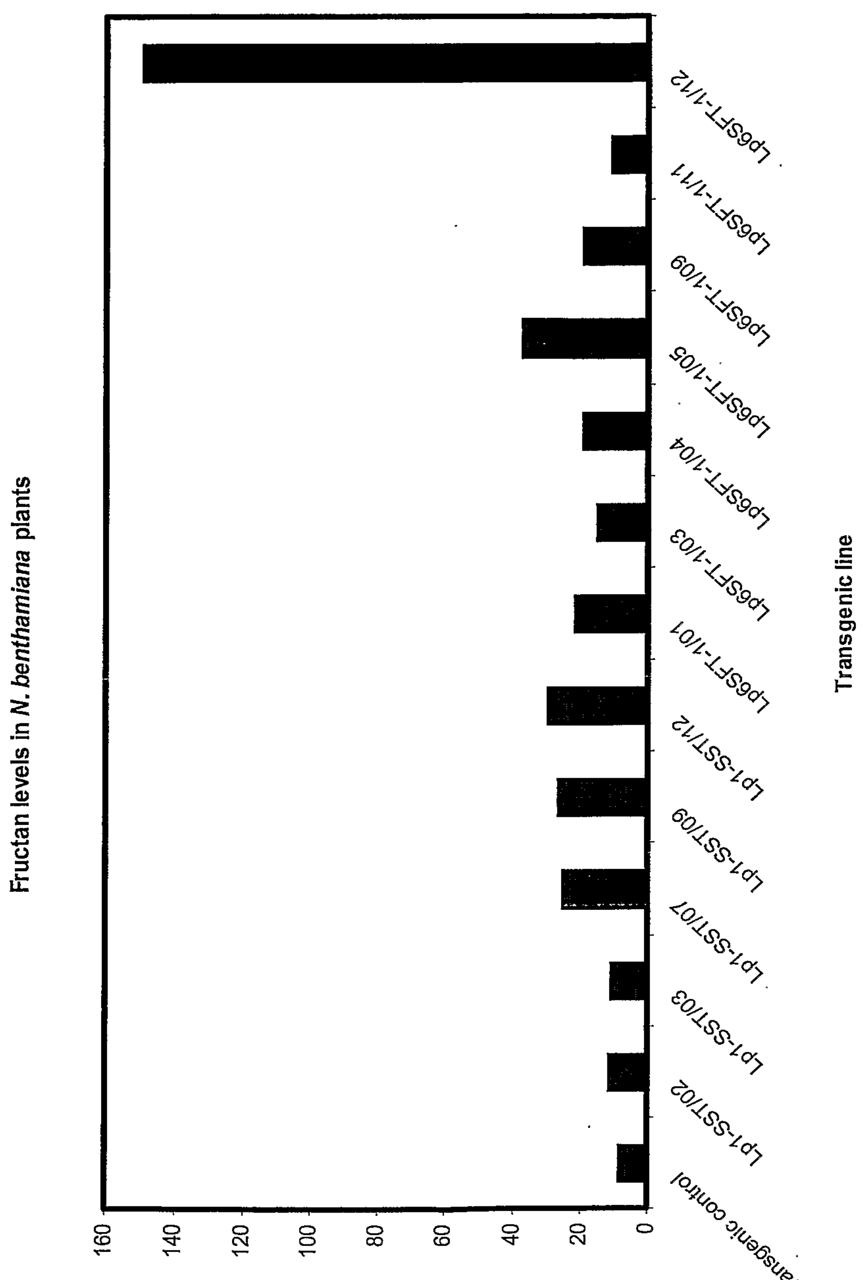
Fructan levels in N. benthamiana plants
Fructan (µg fructose/g tissue)
160
140
120
100
80
60
40
20
0
Transgenic control
Lp1-SST/02
Lp1-SST/03
Lp1-SST/07
Lp1-SST/09
Lp1-SST/12
Lp6SFT-1/01
Lp6SFT-1/03
Lp6SFT-1/04
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Lp6SFT-1/11
Lp6SFT-1/12
Transgenic line

Figure 5.

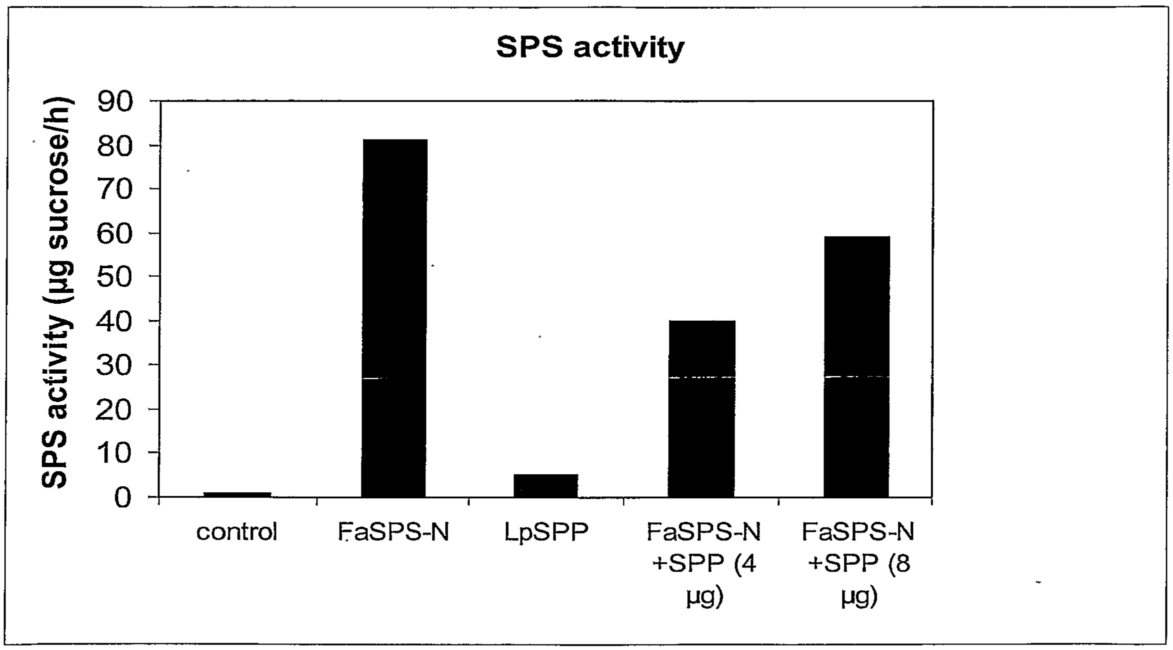
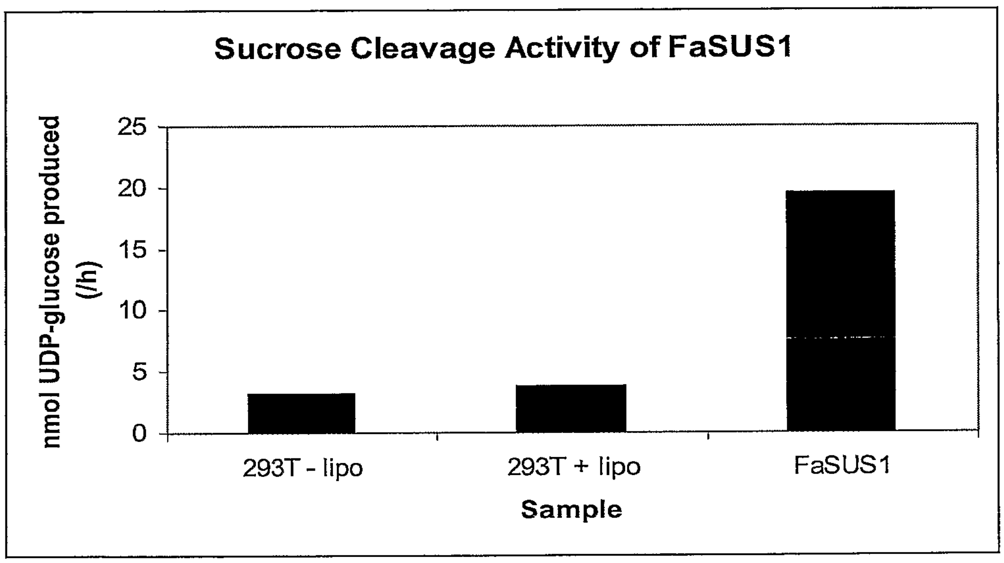
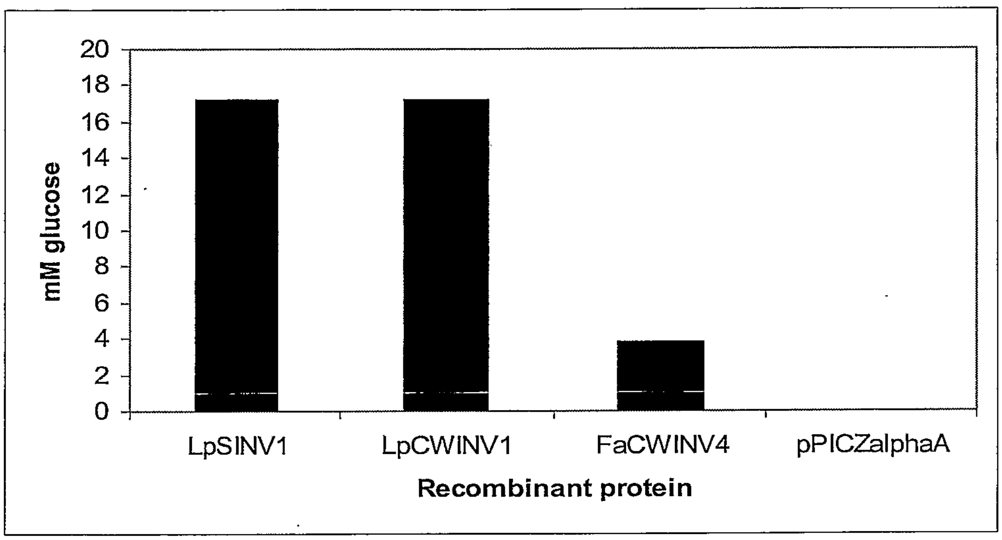

SPS activity
SPS activity (µg sucrose/h)
90
80
70
60
50
40
30
20
10
0
control
FaSPS-N
LpSPP
FaSPS-N +SPP (4 µg)
FaSPS-N +SPP (8 µg)

Figure 6.



Sucrose Cleavage Activity of FaSUS1
nmol UDP-glucose produced (/h)
25
20
15
10
5
0
293T - lipo
293T + lipo
FaSUS1
Sample

Figure 7.


20
18
16
14
12
10
8
6
4
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LpSINV1
LpCWINV1
FaCWINV4
pPICZalphaA
Recombinant protein

Figure 8.

SEQUENCE LISTING

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Gibson, John Bryan
Shenk, Michael Andrew
Norriss, Geoffrey
Glenn, Matthew
Saulsbury, Keith Martin
Hall, Claire

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<213> Festuca arundinacea

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<212> DNA
<213> Festuca arundinacea

<400> 3
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<212> DNA
<213> Lolium perenne

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<211> 2163
<212> DNA
<213> Festuca arundinacea

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<213> Festuca arundinacea

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<213> Festuca arundinacea

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<212> DNA
<213> Festuca arundinacea

<400> 31

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<213> Lolium perenne

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<211> 1775
<212> DNA
<213> Festuca arundinacea

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<212> DNA
<213> Lolium perenne

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aaa 1323

<210> 35
<211> 1313
<212> DNA
<213> Festuca arundinacea

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<212> DNA
<213> Lolium perenne

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<210> 37
<211> 1063
<212> DNA
<213> Festuca arundinacea

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<212> DNA
<213> Lolium perenne

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<212> DNA
<213> Festuca arundinacea

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<211> 1429
<212> DNA
<213> Festuca arundinacea

<400> 40
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<210> 41
<211> 1457
<212> DNA
<213> Lolium perenne

<400> 41
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<210> 42
<211> 1452
<212> DNA
<213> Festuca arundinacea

<400> 42
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<210> 43
<211> 1440
<212> DNA
<213> Lolium perenne

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<210> 44
<211> 2102
<212> DNA
<213> Lolium perenne

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<210> 45
<211> 2051
<212> DNA
<213> Festuca arundinacea

<400> 45
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<211> 2461
<212> DNA
<213> Lolium perenne

<400> 46
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<213> Lolium perenne

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<213> Lolium perenne

<400> 55
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tcaggctcct cttcctctcc cctggccctg gaggcagtcg gtcggatctg gccggtcgcc 180
ggagacgcgc tcggccgtcc actgctcgcc gccgctgcct tctagccact accgttcagc 240
ctccagagcc aagcggcagt ctagcccaac agcaggagcg tagaatagtg ttacctcttg 300
tttcattatt caatatacaa aatggccgtg tcggagcttg aggtcgacgg cgtcgtcttc 360
ccgccgctgg cccgtccgcc gggcacagcc cacgcgcact tcctcgccgg cgcaggtgtg 420
cgagggatgg agctcggcgg caacttcatc aagttcacgg ccatcggcgt gtacctgcag 480
gccgacgccg ccgtgtccgc gctcgccacg aagtgggccg ggaaacccgc cgacgagctt 540
gctgcagaca acgccttctt ccgcgacgtc gtcacaggcg agttcgagaa gttcacgccg 600
gtgaccatga tcctgccgct caccggcgcg cagtactccg agaaggtgac cgagaactgc 660

gtcgcgtact ggaaggccgt cggcaagtac acgaacgccg aggccgccgc cgtcgacaag 720
ttcaaggagg ccttcaggac tgagagcttc cctcccggcg cgtccatcct cttcacccac 780
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cacggggtct cgccggcggc gaagctcagc ctggcgacca gggtcgccga gctcctgaat 960
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cggacaccgt cactgctggc ttgtgtggtt ggcgatgtcc gttgttgaga cgtcgtgttc 1080
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aaccgctgcc caagaaaaaa aaaa 1164

<210> 56
<211> 933
<212> DNA
<213> Festuca arundinacea

<400> 56
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ataccatcgg ccgtctcgga gcttgaggtc gacggcgtcg tcttcccgcc gctggcccgt 120
ccgccgggca cagcccacgc gcacttcctc gccggcgcag gtgtgcgagg gatggagctc 180
ggcggcaact tcatcaagtt cacggccatc ggcgtgtacc tgcaggccga cgccgccgtg 240
tccgcgctcg ccgcgaagtg ggccgggaaa cccgccgacg agcttgccgc agacaacgcc 300
ttcttccgcg acgtcgtcac gggcgagttc gagaagttca ggcgggtgac catgatcctg 360
ccgctcaccg gcgcgcagta ctccgagaag gtgaccgaga actgcgtcgc ctactggaag 420
gccgtcggca agtacacgga cgctgaggcc gccgccgtcg acaagttcaa ggaggccttc 480
aaggccgaga gtttccctcc cggcgcgtcc atcctcttta cccactcccc cgccggcgtc 540
ctcaccgtcg cgttctcgaa agactcgtcg ttgccggagt cgggcggcgt ggcgatagag 600
aacaggccgc tctgcgaggc cgtgctgaag tccatcatcg gcaagcatgg ggtctcgccg 660
gccgcgaagc tcagcctggc gaccagggtc gccgagctcc tgaaggaggc cgcacccgtc 720
ggcgagccgg cggtggcaga gcccgtgtcg gtttcagcat gaacggactg ggcaccgtca 780
ctgctggctt atacatgtgg ttggtgatgt ccgtgttgag acatcgtgtt ccggagcttc 840
taccgttgtt tctcttgcgt ccaggtcaac cgtgctaact tgaataaaga aaccccagcc 900
attgaaattt atttacatca aataaaaaaa aaa 933

<210> 57
<211> 1531
<212> DNA
<213> Lolium perenne

<400> 57
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gccgcgacga tgaccgtgga ggaggtgagg aaggcacagc gggcggaggg gccggcgacg 180
gtgctggcca tcggcacggc gacgcccgct aactgtgtct accaggctga ctacccggac 240
tactacttca agatcaccaa gagcgaccac ctcgccgatc tcaaggagaa gttcaagagg 300
atgtgcgaca agtctcagat caggaagagg tacatgcacc tgacggagga gatcctggag 360
gagaacccca acatgtgcgc gtacatggcg ccgtcgctgg acgcgcgcca ggacatagtt 420
gtcgtcgagg tcccgaagct cgggaaggcg gcggcacaga aggcgatcaa ggagtggggc 480
cagccgcggt ccaagatcac ccacctcgtc ttctgcacta cctctggtgt ggacatgcca 540
ggcgccgact accagctcac caagatgctc ggcctgcgcc cgtcggtgaa gcgcctcatg 600
atgtaccagc agggctgctt cgccggcggc acggtgctcc gcctcgccaa ggacctggct 660
gaaaacaacc gcggcgcgcg cgtgctggtg gtctgctcgg agatcacggc cgtgaccttc 720
cgcggcccgc acgagtcaca cctcgactcg ctggtcggcc aggcgctctt cggggacggc 780
gctgccgcgg tgataatcgg cgccgacccc gacgtgtccg tcgagcgccc gctgttccag 840
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ttttgggtgg cgcacccggg cgggccggcg atcctcgaca tggtggaggc aaaggtaaac 1080
ctcaacaagg agcggatgcg tgccaccagg cacgtcctct ccgagtacgg caacatgtcc 1140
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accaccaccg gcgagggaat ggattggggc gtcctctttg gcttcgggcc cggcctcacc 1260
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gttccatctc cgtttatctg ccacatcgat ggatacctac tactactacc gccgccgccg 1380
ctgctatcca aagtaatttg tattgtattc atgcatacct ggtttgtatt tgttggtagg 1440
attcgttccg ctattatgtc gcttgtgtcg cgtacactgt tgtatcctag taatagtaat 1500
caaacggagt acggtttatg taaaaaaaaa a 1531

<210> 58
<211> 774
<212> DNA
<213> Festuca arundinacea

<400> 58
acagatgtac ttcgtgtcca agtccctggc ggagaacgcc gccatggact acgccaaaga 60
gaacggcgtg gacttcatca gcatcatccc cacgctcgtc gtcggcccct tcctcagcgc 120
cggcatgccg cccagcctgg tcaccgccct ggcactcatc acggggaacg aggcccacta 180
ctcgatcctg aagcaggtgc agctggtcca cctggacgac ctctgcgact ccatgaccta 240
cctcttcgag cacccggacg ccaacggccg ctacatctgc tcctcccacg acaccaccat 300
tcatggcatc gccaggatgc tcaaggagag gttccccgag tacgacatcc cacagaaatt 360
cccgggagcc gacgacgacc ttcagccgat ccacttcttc ttcaagaagc tgctcgacca 420
cgggttcagg ttcaggtaca ccgccgagga catgttcgac gccgcggtct ggacgtgcag 480
ggagaagggc ctgattccgc tcggagcgga aggggcaggc ggcccggcca gtgcagccgg 540
caagctggga gctgttctcg tgggcgaagg tcaggcgatt ggtgctgaga cataagcgct 600
agtgcatgta cactaggctg gctacctcag acacatggtg gagcgatgat tatgttcgtt 660
aattctacta tcctatattt cggttcagaa attgcattaa gagaaccctg taattggtgg 720
gatattatga acggattatg gaacgcaaat aacttcatga cggaaaaaaa aaaa 774

<210> 59
<211> 1211
<212> DNA
<213> Lolium perenne

<400> 59
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cggcttcatc ggctcctggc tcgtccgcct cctcctcgcc cgcggctact ccgtccacgc 120
cgccgtcctc aaccccgatg acaaggccga gacggaccac ctcctcgcgc tcgccgctgc 180
ggccggcgac gagggccgca tccgcttctt caggtgcgac ctcctcgacg gcgccgccat 240
gctcgccgcc gtgcggggat gctccggcgt gttccacctc gcctctccct gcaccgtcaa 300
cctcgtcctc aacccccaaa aggagcttgt ggtgccggcg gtggagggca cgctcaacgt 360
gctgcgcgcc gccaaggaag ctgggggagt gcggcgggtg gtggtgacct cctccgtctc 420
cgccctcgtc ccctgcccgg ggtggccggc cggcgaggtc ctcgacgagc gctgctggac 480
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cttacttgaa ggttgcaaag aggagtatgc agatttcttc atcgggccag tgcacgtgga 720
agacgttgca ttagcccata ttctgctgta cgagaatccg tcagcatccg ggaggcacct 780
ctgcgtggag cccatctgtc actggagtgt tttcgcggcg aaagtcgccg agctctaccc 840
tgattacaaa gttccaaaat tccctgagga cacacagcct gggctggtga gggcgaaggc 900
ggtgccaaaa aagctgatgg cgttgggttt gcagttcact cctcttgaga agatcatcag 960
ggatgccgtg gagagcctca agagcagagg atgcatcgcc tgatgattgg atcgttaggc 1020
atgtcaccct tccgtcgtag gttcatgatc atccttgttg aaaaatgtgt tgtgttgtgt 1080
ccagcccagt gcctacccag accatatact taccagtatg atttgtgcaa taacagccgg 1140
ttgatgtacg gcatcacctg ccctacactt gggatgcgga tgctgtcaca ctgactccct 1200
caaaaaaaaa a 1211

<210> 60
<211> 1229
<212> DNA
<213> Lolium perenne

<400> 60
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atcaagaaac tccttgagtc tggatatcat gtgataggga ctgtcagaga cccagggaat 120
cgaagaaagg tgggacacct ttggaaacta ccaggtgcaa atgagaggct ccaacttgtg 180
agagctgatc tattggagga agggagcttt gacgatgctg taagggcttg tgagggtgtc 240
ttccacattg cgtcgcctgt ccttgggaaa tctgattcca attgcaagga agcaacactc 300
ggtcctgcaa tcaatggtac cctcaacgtg ctaagatcct gcaagaagag tccatttctc 360
aaaagggttg ttctcacatc ttcatcatcc gcggtaagga ttagggatga aactcagcag 420
ccagaactgt tatgggatga aacgacatgg agctctgtgc cactctgtga aaagctacag 480
ctatggtatg ccctggcaaa ggtatttgca gagaaagcag cattggactt tgccaaggag 540
aataacattg accttgtgac agttcttcca tcattcgtaa ttggacccag tttatcccat 600
gaattgtgca ctactgcttc agatatcctt ggcttacttc aaggtgacac agacaggttc 660
actttgtacg gaaggatggg atatgttcac atcgatgatg ttgcccggag ccacattcta 720

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gtgtacgaaa caccggaggc aactggcaga tatctgtgca gctcagtggt tctggataac    780
aatgaattgg ttggcttact ggcaaaacag tttccagtat tccccattcc aaggaggctc    840
aagaacccct atggaaagca ggcataccag ctagacacat ccaagctcca ggggctgggt    900
ctcaagttca aaggagtgca ggagatgttt aacgactgcg tcgaatcgct gaaagatcag    960
ggccatttgc tggagtgccc gttgtgataa cagagacagc attgacaagc catagccaaa   1020
cagcattgac aagccatagc caaacacatc tcaactatgc ctgaatcatg tcagttctcg   1080
agtcatagat tttttttttc tcttcaaata attcccatgt actctcctta ctataccgaa   1140
catcaattgt cagcggcaga ttaaatgtgt ccatatgctt tgcaattgtt tcaattagta   1200
atgaaatatt tgaaacaaaa aaaaaaaaa                                     1229

<210> 61
<211> 1439
<212> DNA
<213> Lolium perenne

<400> 61
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gaggatggcg ccggtggtgg agagagcgcc cttcctgccg acgggggagg ccacgctgcg    120
gccgtccttc gtgcgggacg aggacgagcg gcccaaggtg gcgcacgacc gcttcagcga    180
cgaggtgccc gtcatctcgc tccacggcat cgacgacgcg cggaggaccg agatccggga    240
ccgcgtggcg gcggcgtgcg aggggtgggg catcttccag gtcgtcgacc acggcgtcga    300
cgccgcgctc atcgccgaga tggccaggct ctcgcgcgac ttcttcgcgc tccccgccga    360
ggacaagctc cgctacgaca tgtccggcgg caagaagggc ggattcatcg tctccagcca    420
cctccagggc gagacggtcc aggactggcg ggagatcgtg acctacttct cgtacccggt    480
caaggcgcgg gactacggcc ggtggccgga caagcccgcg ggtggcgcg cggtggtgga    540
gcagtacagc gagcggctca tggcgctgtc ctgcaagctg ctgggggtgc tgtcggaggc    600
catgggcctg gagacggagg ccctgtccaa ggcgtgcgtg gacatggacc agaaggtggt    660
ggtcaacttc taccccaagt gcccccagcc cgacctcacc ctcggcctca agcgccacac    720
cgaccccggc accatcaccc tcctcctcca ggacctcgtc ggcggactcc aggccacccg    780
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ggtgaacggg gagagcagca ggctgtccat cgccacgttc cagaacccgg cgcccgacgc    960
caaggtgtgg ccgctggcgg tgagggaggg ggaggacacc atcctggagg agcccatcac   1020
cttcaccgag atgtaccgcc gcaagatggc gcgcgacctc gagctcgcca agcgcaagaa   1080
gcaggccaag gccgatcagc tcaagcagca gctgcagcag gaggccgcgc ccgccgccgc   1140
gcccaccaag ccactcaacc agattcttgc ctagattcca tgccgattca ttcatgcgtg   1200
atatatagta ctatgtacta tatcgtatta aaataagtaa ttatctctat ctactcattt   1260
gtgtgtaatt aagagatgag taattatcta gtatatacac atttgtctgc gaggagcgag   1320
ctggacctgt aataacatgt agcatgtcct acgtggaacc gatcagctga ttggagctgt   1380
cacatgagtt tgctgtgtgc agaaattgaa cgcattcggt actgctttca aaaaaaaaa    1439

<210> 62
<211> 1320
<212> DNA
<213> Festuca arundinacea

<400> 62
gaaacggccc tgcactagac gaaccagaca aacgactcca tcccacagac gactcgccgg     60
ccgccacgcc cacgcaccac tttacggggc cgatcggatc ggatggcgtc ggtggagaac    120
gcgccgttcc tgccgacggc ggcgacgggc gaggccacgc tgcggccgtc cttcgtgcgg    180
gacgaggacg agcgacccaa ggtggcgcac gaccgcttca gcgacgaggt gccggtcatc    240
tcgctccacg gcatcgatga tggcggcgcg cggagggccg agatccggga ccgcgtggcg    300
gcggcgtgcg aagggtgggg cgtcttccag gtcgtcgacc acggcgtcga cgccgccctc    360
gtcgccgaga tggccaggct ctcccgcgag ttcttcgcac tccccgccga ggacaagctc    420
cgctacgaca tgtccggcgg caagaaaggt ggattcatcg tctccagcca cctccagggc    480
gagacggtcc aggactggcg ggagatcgtg acctacttct cgtacccggt gaaggcgcgg    540
gactacggcc ggtggccgga gaagcctgcg ggtggcgcg cggtggtgga gcagtacagc    600
gagcggctca tggcgctgtc gtgcaagctg ctgggggtgc tgtcggaagc catgggcctg    660
gagacggagg ccctgtccaa ggcgtgcgtg gacatggacc agaaggtggt ggtcaacttc    720
taccccaagt gcccccagcc cgacctcacc ctcgggctca agcgccacac cgaccccggc    780
accatcaccc tcctcctcca ggacctcgtc ggcggactcc aggccactcg cgacggcggc    840
aacacctgga tcaccgtgca gcccgtcccc ggcgccttcg tcgtcaacct cggcgaccac    900
ggccactact tgagcaacgg gaggtttaag aacgcggacc accaggcggt ggtcaacggg    960
gagagcagca ggctgtccat cgccacgttc cagaacccgg cgccagaagc gaaggtgtgg   1020
ccgctggcgg taagggaggg ggaggacacc atactggagg agcccatcac cttcaccgag   1080
atgtaccgcc gcaagatggc gtgcgacctc gagctcgcca agcgcaagaa gcaggccaag   1140
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gccgaccagc tcaagcagca gctgcagcag gagcagcagg aggcggtggc cgccgccgcg 1200
cccaagcccg ccaccaccaa gcccctcaac cagattcttg cctagattcc atgtatatgt 1260
atatcgtatt aaaataagaa attatctata tatatatata tatatataaa aaaaaaaaaa 1320

<210> 63
<211> 654
<212> PRT
<213> Lolium perenne

<400> 63
Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Pro Leu Leu Pro
1 5 10 15
Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Ser Asp Asp Ala Arg Glu Asn
20 25 30
Arg Ser Ser Gly Gly Val Arg Trp Arg Ala Cys Ala Val Val Leu Ala
35 40 45
Asp Ser Ala Leu Ala Val Val Val Val Val Gly Leu Leu Ala Gly Gly
50 55 60
Arg Val Asp Arg Val Pro Ala Gly Ala Asp Val Ala Ser Ala Thr Val
65 70 75 80
Pro Ala Val Pro Met Glu Phe Pro Arg Ser Arg Gly Lys Asp Leu Gly
85 90 95
Val Ser Glu Lys Ser Ser Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro
100 105 110
Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe Gln
115 120 125
Pro Glu Gln His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly
130 135 140
Gly Trp Tyr His Leu Phe Tyr Gln His Asn Pro Lys Gly Asp Ser Trp
145 150 155 160
Gly Asn Ile Ala Trp Ala His Ala Val Ser Lys Asp Met Val Asn Trp
165 170 175
Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ser Asn
180 185 190
Gly Val Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Gln Val Ile
195 200 205
Leu Leu Tyr Thr Gly Asn Thr Asp Thr Leu Ala Gln Val Gln Cys Leu
210 215 220
Ala Thr Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys
225 230 235 240
His Pro Ala Asn Pro Ile Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys
245 250 255
Asp Phe Arg Asp Pro Leu Thr Ala Trp Phe Asp His Ser Asp His Thr
260 265 270
Trp Arg Thr Val Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile
275 280 285
Ile Leu Ser Tyr Lys Thr Lys Asp Phe Val Asn Tyr Glu Leu Met Pro
290 295 300
Gly Asn Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile
305 310 315 320
Asp Leu Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp
325 330 335
Asp Ser Pro Asp Val Leu Phe Val Leu Lys Glu Ser Ser Asp Asp Glu
340 345 350
Arg His Asp Tyr Tyr Ala Leu Gly Arg Phe Asp Ala Val Ala Asn Val
355 360 365
Trp Thr Pro Ile Asp Arg Asp Leu Asp Leu Gly Ile Gly Leu Arg Tyr
370 375 380
Asp Trp Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Gln Lys Lys
385 390 395 400
Asn Arg Arg Ile Val Trp Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln
405 410 415
Ala Asp Ile Thr Lys Gly Trp Ala Asn Leu Met Thr Ile Pro Arg Thr
420 425 430
Val Glu Leu Asp Arg Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val
435 440 445

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Glu Glu Val Asp Thr Leu Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile
    450                 455                 460
Thr Val Asn Ala Gly Ser Val Ile Arg Leu Pro Leu His Gln Gly Ala
465                 470                 475                 480
Gln Leu Asp Ile Glu Ala Ser Phe Gln Leu Asn Ser Ser Asp Val Asp
                485                 490                 495
Ala Ile Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala
            500                 505                 510
Ala Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Leu Ala Asn
        515                 520                 525
Gly Arg Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Val
    530                 535                 540
Asp Gly Gly Leu Gln Thr His Phe Cys His Asp Glu Ser Arg Ser Thr
545                 550                 555                 560
Arg Ala Lys Asp Val Val Asn Arg Met Ile Gly Ser Ile Val Pro Val
                565                 570                 575
Leu Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile
            580                 585                 590
Val Gln Ser Phe Ala Met Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala
        595                 600                 605
Tyr Pro Thr Glu Thr Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn
    610                 615                 620
Asn Ala Thr Gly Ala Thr Val Thr Ala Glu Arg Leu Val Val His Glu
625                 630                 635                 640
Met Ala Ser Ala Asp Asn His Ile Phe Thr Asn Asp Asp Leu
                645                 650
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<210> 64
<211> 648
<212> PRT
<213> Festuca arundinacea

<400> 64

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Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Ala Asp Asp Ala Arg Glu Asn
            20                  25                  30
Gln Gly Ser Asp Gly Val Arg Trp Arg Ala Cys Ala Ala Val Leu Ala
        35                  40                  45
Ala Ser Ala Leu Ala Val Leu Val Val Val Gly Leu Leu Ala Gly Gly
    50                  55                  60
Arg Val Asp Arg Pro Gly Pro Ala Ala Val Pro Ala Val Pro Thr Glu
65                  70                  75                  80
Ile Pro Arg Ser Arg Gly Lys Asp Phe Gly Val Ser Glu Lys Ser Ser
                85                  90                  95
Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro Trp Ser Asn Ala Met Leu
            100                 105                 110
Gln Trp Gln Arg Thr Gly Phe His Phe Gln Pro Glu Gln His Tyr Met
        115                 120                 125
Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp Tyr His Leu Phe
    130                 135                 140
Tyr Gln Tyr Asn Pro Lys Gly Asp Ser Trp Gly Asn Ile Ala Trp Ala
145                 150                 155                 160
His Ala Val Ser Lys Asp Met Val Asn Trp Arg His Leu Pro Leu Ala
                165                 170                 175
Met Val Pro Asp Gln Trp Tyr Asp Ser Asn Gly Val Leu Thr Gly Ser
            180                 185                 190
Ile Thr Val Leu Pro Asp Gly Arg Val Ile Leu Leu Tyr Thr Gly Asn
        195                 200                 205
Thr Asp Thr Leu Ala Gln Val Gln Cys Leu Ala Glu Pro Ala Asp Pro
    210                 215                 220
Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys His Pro Ala Asn Pro Ile
225                 230                 235                 240
Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys Asp Phe Arg Asp Pro Leu
                245                 250                 255
Thr Asp Trp Phe Asp His Ser Asp Asp Thr Trp Arg Thr Val Ile Gly
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                260                     265                     270
Ser Lys Asp Asp Asp Gly His Ala Gly Ile Ile Leu Ser Tyr Lys Thr
            275                 280                     285
Lys Asp Phe Val Asn Tyr Glu Leu Met Pro Gly Asn Met His Arg Gly
    290                 295                     300
Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile Asp Leu Tyr Pro Val Gly
305                 310                     315                 320
Gly Asn Ser Ser Glu Met Leu Gly Gly Asp Asp Ser Pro Asp Val Leu
                325                     330                 335
Phe Val Leu Lys Glu Ser Ser Asp Asp Glu Arg His Asp Tyr Tyr Ala
            340                 345                     350
Leu Gly Arg Phe Asp Ala Ala Ala Asn Ile Trp Thr Pro Ile Asp Gln
        355                 360                     365
Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Tyr Tyr
    370                 375                     380
Ala Ser Lys Ser Phe Tyr Asp Gln Arg Lys Asn Arg Arg Val Val Trp
385                 390                     395                 400
Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln Ala Asp Ile Thr Lys Gly
                405                     410                 415
Trp Ala Asn Leu Met Thr Ile Pro Arg Thr Val Glu Leu Asp Lys Lys
            420                 425                     430
Thr Arg Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Val Asp Thr Leu
        435                 440                     445
Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile Thr Val Asn Ala Gly Ser
    450                 455                     460
Val Ile Arg Leu Pro Leu His Gln Gly Ala Gln Leu Asp Ile Glu Ala
465                 470                     475                 480
Ser Phe Gln Leu Asn Ser Ser Asp Val Asp Ala Leu Asn Glu Ala Asp
                485                     490                 495
Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala Ala Val Arg Gly Ala Leu
            500                 505                     510
Gly Pro Phe Gly Leu Leu Val Leu Ala Asn Gly Arg Thr Glu Gln Thr
        515                 520                     525
Ala Val Tyr Phe Tyr Val Ser Lys Gly Val Asp Gly Ala Leu Gln Thr
    530                 535                     540
His Phe Cys His Asp Glu Ser Arg Ser Thr Arg Ala Lys Asp Val Val
545                 550                     555                 560
Asn Arg Met Ile Gly Ser Ile Val Pro Val Leu Asp Gly Glu Thr Phe
                565                     570                 575
Ser Val Arg Val Leu Leu Asp His Ser Ile Val Gln Ser Phe Ala Met
            580                 585                     590
Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala Tyr Pro Thr Glu Ala Ile
        595                 600                     605
Tyr Ala Ala Ala Gly Val Tyr Val Phe Asn Asn Ala Thr Gly Ala Thr
    610                 615                     620
Val Thr Ala Glu Arg Leu Val Val Tyr Glu Met Ala Ser Ala Asp Asn
625                 630                     635                 640
His Ile Phe Arg Asn Asp Asp Leu
                645
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<210> 65
<211> 620
<212> PRT
<213> Festuca arundinacea

<400> 65

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Met Glu Ser Arg Ala Phe Pro Asn Ala Ala Tyr Ala Pro Leu Leu Pro
1               5                   10                  15
Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
            20                  25                  30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
        35                  40                  45
Leu Leu Val Ala Ala Thr Met Leu Ala Gly Ser Arg Met Gly Gln Ala
    50                  55                  60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
65                  70                  75                  80
```

Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
85 90 95

Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
100 105 110

Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
115 120 125

Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
130 135 140

Pro Leu Ala Leu Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
145 150 155 160

Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
165 170 175

Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
180 185 190

Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
195 200 205

Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
210 215 220

Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp Ala Thr Trp Arg
225 230 235 240

Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
245 250 255

Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
260 265 270

Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
275 280 285

Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
290 295 300

Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
305 310 315 320

Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
325 330 335

Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
340 345 350

Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
355 360 365

Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
370 375 380

Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu Asp Glu Lys Thr
385 390 395 400

Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
405 410 415

Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Asp Asn Gly Ser Val
420 425 430

Phe His Leu Pro Leu His Gln Ala Thr His Leu Asp Ile Glu Ala Ser
435 440 445

Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
450 455 460

Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala Arg Gly Ala Ile
465 470 475 480

Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
485 490 495

Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Thr Leu
500 505 510

Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
515 520 525

Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu His Gly Glu
530 535 540

Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
545 550 555 560

Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
565 570 575

Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
580 585 590

Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
595 600 605

Val Tyr Asp Glu Thr Leu Ile Met Val Glu Asp Ser
610 615 620

<210> 66
<211> 623
<212> PRT
<213> Lolium perenne

<400> 66
Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
1 5 10 15
Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
20 25 30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
35 40 45
Leu Leu Val Gly Ala Thr Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
50 55 60
Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
65 70 75 80
Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
85 90 95
Pro Glu Gly His Phe Met Ser Asp Pro Asn Gly Pro Val Tyr Tyr Arg
100 105 110
Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
115 120 125
Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
130 135 140
Trp Arg Pro Leu Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys
145 150 155 160
Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
165 170 175
Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
180 185 190
Cys Ile Ala Val Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp
195 200 205
Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
210 215 220
Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp
225 230 235 240
Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
245 250 255
His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
260 265 270
Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
275 280 285
Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
290 295 300
Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
305 310 315 320
Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
325 330 335
Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
340 345 350
Lys Leu Tyr Ala Ser Thr Ser Phe Tyr Asp Pro Val Lys Gln Arg Arg
355 360 365
Ile Met Leu Gly Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val
370 375 380
Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu
385 390 395 400
Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
405 410 415
Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
420 425 430
Asn Gly Ser Val Phe His Leu Pro Leu His Gln Thr Thr Gln Leu Asp
435 440 445

Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
450 455 460
Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
465 470 475 480
Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
485 490 495
Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
500 505 510
Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
515 520 525
Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
530 535 540
Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
545 550 555 560
Val Gln Ser Phe Ala Met Gly Gly Arg Thr Thr Ala Thr Ser Arg Val
565 570 575
Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
580 585 590
Asn Ala Thr Gly Ala Gly Val Thr Ala Glu Arg Leu Ile Val His Glu
595 600 605
Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Glu Asp Ser
610 615 620

<210> 67
<211> 623
<212> PRT
<213> Festuca arundinacea

<400> 67
Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
1 5 10 15
Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
20 25 30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
35 40 45
Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
50 55 60
Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
65 70 75 80
Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
85 90 95
Pro Glu Gly His Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg
100 105 110
Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
115 120 125
Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
130 135 140
Trp Arg Pro Leu Pro Val Ala Met Arg Pro Asp His Trp Tyr Asp Lys
145 150 155 160
Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
165 170 175
Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
180 185 190
Cys Ile Ala Val Pro Thr Asp Pro Asn Asn Pro Leu Leu Arg His Trp
195 200 205
Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
210 215 220
Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp
225 230 235 240
Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
245 250 255
His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
260 265 270
Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
275 280 285

Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
290 295 300
Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
305 310 315 320
Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
325 330 335
Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
340 345 350
Lys Leu Tyr Ala Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg
355 360 365
Ile Met Leu Gly Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val
370 375 380
Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu
385 390 395 400
Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
405 410 415
Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
420 425 430
Asn Gly Ser Val Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp
435 440 445
Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
450 455 460
Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
465 470 475 480
Arg Gly Ala Ile Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
485 490 495
Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
500 505 510
Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
515 520 525
Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
530 535 540
Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
545 550 555 560
Val Gln Ser Phe Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val
565 570 575
Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
580 585 590
Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu
595 600 605
Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Gln Asp Ser
610 615 620

<210> 68
<211> 619
<212> PRT
<213> Lolium perenne

<400> 68
Met Glu Ser Arg Asp Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
1 5 10 15
Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
20 25 30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
35 40 45
Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
50 55 60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
65 70 75 80
Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
85 90 95
Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
100 105 110
Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
115 120 125

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Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
    130                 135                 140
Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
145                 150                 155                 160
Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
                165                 170                 175
Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
            180                 185                 190
Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
        195                 200                 205
Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
    210                 215                 220
Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp Ser Thr Trp Arg
225                 230                 235                 240
Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
                245                 250                 255
Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ile Phe Glu Arg Val Pro
            260                 265                 270
Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
        275                 280                 285
Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
    290                 295                 300
Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
305                 310                 315                 320
Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
                325                 330                 335
Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
            340                 345                 350
Ser Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
        355                 360                 365
Tyr Val Gly Asp Val Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
    370                 375                 380
Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu Asp Glu Lys Thr
385                 390                 395                 400
Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
                405                 410                 415
Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Glu Asn Gly Ser Ile
            420                 425                 430
Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
        435                 440                 445
Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
    450                 455                 460
Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala Arg Gly Ala Leu
465                 470                 475                 480
Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
                485                 490                 495
Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Ser Leu
            500                 505                 510
Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
        515                 520                 525
Val Ala Lys Arg Val Val Gly Ser Thr Val Pro Val Leu Asp Gly Glu
    530                 535                 540
Val Leu Ala Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
545                 550                 555                 560
Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
                565                 570                 575
Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
            580                 585                 590
Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
        595                 600                 605
Val Tyr Asp Glu Thr Val Met Val Lys Asp Ser
    610                 615
```

<210> 69
<211> 422

<212> PRT
<213> Festuca arundinacea

<400> 69
Met Asp Lys Leu Asn Gly Ser Ala Arg Leu Met Ile Val Ser Asp Leu
1   5   10   15
Asp His Thr Met Val Asp His His Asp Glu Glu Asn Leu Ser Leu Leu
            20   25   30
Arg Phe Gly Ala Leu Trp Glu Ser Ala Tyr Cys Gln Asp Ser Leu Leu
        35   40   45
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
    50   55   60
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Ser
65   70   75   80
Glu Ile Thr Tyr Gly Glu Ala Met Val Pro Asp Asp Gly Trp Glu Glu
                85   90   95
Tyr Leu Asn Asn Lys Trp Asp Arg Asn Ile Val Leu Glu Glu Thr Ala
            100   105   110
Lys Tyr Ser Glu Leu Lys Leu Gln Pro Glu Thr Glu Gln Arg Pro His
        115   120   125
Lys Val Ser Phe Leu Val Asp Lys Lys Ser Ala Gln Glu Val Ile Lys
    130   135   140
Ser Leu Ser Glu Lys Phe Glu Lys Arg Gly Val Asp Ala Lys Ile Ile
145   150   155   160
Tyr Ser Gly Gly Gln Asp Leu Asp Ile Leu Ala Gln Gly Ala Gly Lys
                165   170   175
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Phe Ala Ser Cys Gly Lys
            180   185   190
Thr Pro Asn Asn Thr Leu Val Cys Gly Asp Ser Gly Asn Asp Ala Glu
        195   200   205
Leu Phe Ser Ile Pro Gly Val His Gly Val Met Val Ser Asn Ala Gln
    210   215   220
Glu Glu Leu Leu Gln Trp His Ala Glu Asn Ala Lys Asp Asn Pro Lys
225   230   235   240
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
                245   250   255
Gly His Phe Lys Leu Gly Pro Asn Ile Ser Pro Arg Asp Ile Glu Phe
            260   265   270
Pro Tyr Val Lys Glu Asp Ser Phe Lys Pro Thr Ala Ala Val Val Lys
        275   280   285
Phe Tyr Val Leu Cys Glu Lys Trp Arg Arg Ala Asp Val Pro Lys Ala
    290   295   300
Asp Ser Val Ile Glu Tyr Phe Lys Asn Ile Thr Asp Ala Ser Gly Val
305   310   315   320
Ile Ile His Pro Ser Gly Leu Glu Leu Ser Ile His Ser Ser Ile Asp
                325   330   335
Ala Leu Ala Ser Cys Tyr Gly Asp Lys Gln Gly Lys Lys Tyr Arg Ser
            340   345   350
Trp Val Asp Arg Leu Val Ile Ser Gln Thr Ala Ser Asp Ser Trp Leu
        355   360   365
Val Arg Phe Asp Leu Trp Glu Ala Glu Gly Asp Ala Trp Val Cys Cys
    370   375   380
Leu Thr Thr Leu Ala Leu Asn Val Lys Pro Glu Thr Pro Gly Gly Phe
385   390   395   400
Val Val Thr His Ile His Lys Thr Trp Leu Lys Glu Tyr Ser Gly Asp
                405   410   415
Glu Gln Ala Ser Lys Leu
            420

<210> 70
<211> 422
<212> PRT
<213> Lolium perenne

<400> 70
Met Asp Lys Leu Asn Gly Ser Ala Arg Leu Met Ile Val Ser Asp Leu
1 5 10 15
Asp His Thr Met Val Asp His His Asp Glu Glu Asn Leu Ser Leu Leu
20 25 30
Arg Phe Gly Ala Leu Trp Glu Ser Thr Tyr Cys Gln Asp Ser Leu Leu
35 40 45
Val Phe Ser Thr Gly Arg Ser Pro Thr Leu Tyr Lys Glu Leu Arg Lys
50 55 60
Glu Lys Pro Met Leu Thr Pro Asp Ile Thr Ile Met Ser Val Gly Ser
65 70 75 80
Glu Ile Thr Tyr Gly Glu Ala Met Val Pro Asp Asp Gly Trp Glu Glu
85 90 95
Tyr Leu Asn Asn Lys Trp Asp Lys Ser Ile Val Leu Glu Glu Thr Ala
100 105 110
Lys Phe Ser Glu Leu Lys Leu Gln Ala Glu Thr Glu Gln Arg Pro His
115 120 125
Lys Val Ser Phe Leu Val Asp Lys Lys Thr Ala Gln Glu Val Ile Lys
130 135 140
Ser Leu Ser Glu Lys Phe Glu Lys Arg Gly Val Asp Ala Lys Ile Ile
145 150 155 160
Tyr Ser Gly Gly Gln Asp Leu Asp Ile Leu Ala Gln Gly Ala Gly Lys
165 170 175
Gly Gln Ala Leu Ala Tyr Leu Leu Lys Lys Phe Ala Ser Cys Gly Lys
180 185 190
Thr Pro Asn Asn Thr Leu Val Cys Gly Asp Ser Gly Asn Asp Ala Glu
195 200 205
Leu Phe Ser Ile Pro Gly Val His Gly Val Met Val Ser Asn Ala Gln
210 215 220
Glu Glu Leu Leu Gln Trp Arg Ala Glu Asn Ala Lys Asp Asn Pro Lys
225 230 235 240
Val Ile His Ala Thr Glu Arg Cys Ala Ala Gly Ile Ile Gln Ala Ile
245 250 255
Gly His Phe Lys Leu Gly Pro Asn Val Ser Pro Arg Asp Val Glu Phe
260 265 270
Pro Tyr Val Lys Glu Asp Ser Phe Lys Pro Thr Ala Ala Val Val Lys
275 280 285
Phe Tyr Val Leu Cys Glu Lys Trp Arg Arg Ala Asp Val Pro Lys Thr
290 295 300
Asp Ser Val Ile Glu Tyr Phe Lys Asn Ile Thr Asp Ala Ser Gly Val
305 310 315 320
Ile Ile His Pro Ser Gly Leu Glu Leu Ser Ile His Ser Ser Ile Asp
325 330 335
Ala Leu Ala Ser Cys Tyr Gly Asp Lys Gln Gly Lys Lys Tyr Arg Ser
340 345 350
Trp Val Asp Arg Leu Val Ile Ser Gln Thr Ala Ser Asp Ser Trp Leu
355 360 365
Val Arg Phe Asp Leu Trp Glu Ala Glu Gly Asp Lys Trp Val Cys Cys
370 375 380
Leu Thr Thr Leu Ala Leu Asn Val Lys Pro Glu Thr Pro Gly Gly Phe
385 390 395 400
Val Val Thr His Ile His Lys Thr Trp Leu Lys Glu Tyr Ser Gly Asp
405 410 415
Glu Gln Ala Ser Lys Leu
420

<210> 71
<211> 1062
<212> PRT
<213> Festuca arundinacea

<400> 71
Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
1 5 10 15
Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
20 25 30

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Glu Thr Ala Pro Ala Leu Ala Ala Glu Glu Ser Gly Ala Ala Tyr Asn
        35                  40                  45
Pro Thr Arg Tyr Phe Val Glu Glu Val Val Arg Ser Phe Asp Glu Gln
    50                  55                  60
Ala Leu His Lys Thr Trp Thr Lys Val Val Ala Met Arg Asn Ser Gln
65                  70                  75                  80
Glu Arg Ser Asn Arg Leu Glu Asn Leu Cys Trp Arg Ile Trp Asn Val
                85                  90                  95
Ser Arg Gln Lys Lys Gln Val Glu Trp Asp Tyr Thr Lys Glu Val Ala
            100                 105                 110
Arg Arg Lys Leu Glu Gln Glu Leu Gly Ser Arg Glu Ala Ala Glu Asp
        115                 120                 125
Leu Ser Glu Leu Ser Glu Gly Glu Lys Asp Thr Thr Thr Ala Lys Pro
    130                 135                 140
Asp Ala Ala Thr Ala Gln Pro Ser Thr Asp Asp Gly Glu His Gln Gln
145                 150                 155                 160
Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
                165                 170                 175
Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
            180                 185                 190
Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
        195                 200                 205
Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
    210                 215                 220
Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
225                 230                 235                 240
Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
                245                 250                 255
Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Glu Asp Asp
            260                 265                 270
Gly Glu Gln Ser Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
        275                 280                 285
Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
    290                 295                 300
Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
305                 310                 315                 320
Leu Gly Asp Gln Leu Gln Pro Pro Pro Thr Pro Ala Ala Gly Asp Gly
                325                 330                 335
Ala Ala Leu Val Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His
            340                 345                 350
Tyr Ala Asp Ala Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn
        355                 360                 365
Val Pro Met Val Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu
    370                 375                 380
Gln Leu Leu Lys Leu Gly Arg Met Pro Gly Pro Glu Ile Gln Gly Thr
385                 390                 395                 400
Tyr Lys Ile Ala Arg Arg Ile Glu Ala Glu Glu Thr Gly Leu Asp Thr
                405                 410                 415
Ala Glu Met Val Val Thr Ser Thr Lys Gln Glu Ile Glu Glu Gln Trp
            420                 425                 430
Gly Leu Tyr Asp Gly Phe Asp Leu Met Val Glu Arg Lys Leu Arg Val
        435                 440                 445
Arg Gln Arg Arg Gly Val Ser Ser Leu Gly Arg Tyr Met Pro Arg Met
    450                 455                 460
Ala Val Ile Pro Pro Gly Met Asp Phe Ser Phe Val Glu Thr Gln Asp
465                 470                 475                 480
Thr Ala Glu Gly Asp Gly Ala Asp Leu Gln Met Leu Ile Ala Pro Asp
                485                 490                 495
Lys Ala Lys Lys Ala Leu Pro Pro Ile Trp Ser Asp Val Leu Arg Phe
            500                 505                 510
Phe Thr Asn Pro His Lys Pro Met Ile Leu Ala Leu Ser Arg Pro Asp
        515                 520                 525
Pro Lys Lys Asn Val Thr Thr Leu Leu Lys Ala Tyr Gly Glu Ser Arg
    530                 535                 540
Gln Leu Arg Glu Leu Ala Asn Leu Thr Leu Ile Leu Gly Asn Arg Asp
545                 550                 555                 560
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Asp Ile Glu Asp Met Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val
565 570 575
Leu Lys Leu Ile Asp Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro
580 585 590
Lys His His Lys Gln Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala
595 600 605
Lys Thr Lys Gly Val Phe Thr Asn Pro Ala Leu Val Glu Pro Phe Gly
610 615 620
Leu Thr Ile Ile Glu Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr
625 630 635 640
Lys Asn Gly Gly Pro Val Asp Ile Leu Lys Ala Leu Asn Asn Gly Leu
645 650 655
Leu Val Asp Pro His Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser
660 665 670
Leu Leu Ala Glu Lys Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu
675 680 685
Arg Asn Ile His Arg Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu
690 695 700
Ser His Val Ser Thr Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu
705 710 715 720
Arg Val Pro Leu Gly Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp
725 730 735
Ser Leu Ser Asp Ser Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp
740 745 750
Ala Ser Ser Asp Leu Asn Ala Ala Asp Ser Ala Ala Ala Ile Met Asp
755 760 765
Ala Leu Arg Arg Arg Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala
770 775 780
Arg Ala Leu Gly Phe Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val
785 790 795 800
Ala Val Asp Cys Tyr Gly Asp Asp Gly Lys Pro Asp Val Lys Gln Leu
805 810 815
Lys Lys Ala Ile Asp Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala
820 825 830
Lys Gln Gly Tyr Val Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala
835 840 845
Glu Ala Ile Lys Ala Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu
850 855 860
Ile Cys Ser Ser Gly Ala Glu Leu Cys Tyr Pro Trp Lys Glu Leu Ala
865 870 875 880
Ala Asp Glu Glu Tyr Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp
885 890 895
His Val Lys Ser Ala Val Pro Arg Leu Gly Ser Leu Glu Glu Ile Ala
900 905 910
Leu Ala Ile Asp Arg Pro Ala Cys Ser Val His Cys His Ala Tyr Ala
915 920 925
Ala Thr Asp Ala Ser Lys Val Lys Lys Val Asp Ser Ile Arg Lys Ser
930 935 940
Leu Arg Met Arg Gly Phe Arg Cys Asn Leu Val Tyr Thr Arg Ala Cys
945 950 955 960
Thr Arg Leu Asn Val Ile Pro Leu Ser Ala Ser Arg Pro Arg Ala Leu
965 970 975
Arg Tyr Leu Ser Ile Gln Trp Gly Ile Asp Leu Ser Lys Val Ala Val
980 985 990
Leu Val Gly Glu Thr Gly Asp Thr Asp Arg Glu Arg Leu Leu Pro Gly
995 1000 1005
Val His Lys Thr Leu Ile Leu Pro Gly Met Val Ala Arg Gly Ser Glu
1010 1015 1020
Glu Leu Leu Arg Gly Asp Asp Gly Tyr Thr Met Ala Asp Val Val Ala
1025 1030 1035 1040
Met Asp Ser Pro Asn Ile Val Thr Leu Ala Glu Gly Gln Ser Ala Ser
1045 1050 1055
Asp Leu Leu Lys Ala Ile
1060

<210> 72
<211> 1074
<212> PRT
<213> Lolium perenne

<400> 72
Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp
1 5 10 15
Ala Gly Gly Thr Ala Gly Asp Ile Ser Ala Ala Ser Val Ala Gly Gly
20 25 30
Asp Asp Gly Pro Gly Ala Gly Gly Gly Thr Ala Gly Glu Lys Arg Asp
35 40 45
Lys Ser Ser Leu Met Leu Arg Glu Arg Gly Arg Phe Asn Pro Ala Arg
50 55 60
Tyr Phe Val Glu Glu Val Ile Ser Gly Phe Asp Glu Thr Asp Leu Tyr
65 70 75 80
Lys Thr Trp Val Arg Thr Ser Ala Met Arg Ser Pro Gln Glu Arg Asn
85 90 95
Thr Arg Leu Glu Asn Met Ser Trp Arg Ile Trp Asn Leu Ala Arg Lys
100 105 110
Lys Lys Gln Ile Glu Gly Glu Glu Ala Ser Arg Leu Ser Lys Lys Arg
115 120 125
Leu Glu Arg Glu Lys Ala Arg Arg Asp Ala Ala Ala Asp Leu Ser Glu
130 135 140
Asp Leu Ser Glu Gly Glu Lys Gly Glu Asn Ile Asn Gly Ser Ser Val
145 150 155 160
His Asp Glu Ser Thr Arg Gly Arg Met Pro Arg Ile Gly Ser Thr Asp
165 170 175
Ala Ile Glu Val Trp Ala Asn Gln His Lys Asp Lys Lys Leu Tyr Ile
180 185 190
Val Leu Ile Ser Ile His Gly Leu Ile Arg Gly Glu Asn Met Glu Leu
195 200 205
Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
210 215 220
Ala Arg Ala Leu Gly Glu Thr Pro Gly Val Tyr Arg Val Asp Leu Leu
225 230 235 240
Thr Arg Gln Ile Ser Ala Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro
245 250 255
Thr Glu Met Leu Ser Pro Arg Asn Ser Glu Asn Leu Gly Asp Asp Met
260 265 270
Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly Pro Arg
275 280 285
Glu Lys Tyr Ile Pro Lys Glu Gln Leu Trp Pro His Ile Gln Glu Phe
290 295 300
Val Asp Gly Ala Leu Val His Ile Met Gln Met Ser Lys Val Leu Gly
305 310 315 320
Glu Gln Val Gly Arg Glu Arg Arg Val Trp Pro Val Val Ile His Gly
325 330 335
His Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
340 345 350
Asn Val Pro Met Val Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu
355 360 365
Glu Gln Leu Leu Lys Gln Gly Arg Gln Thr Arg Asp Glu Val Asn Ala
370 375 380
Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Cys Leu Asp
385 390 395 400
Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Glu Lys Gln
405 410 415
Trp Gly Leu Tyr Asn Gly Phe Asp Val Thr Met Glu Arg Lys Leu Arg
420 425 430
Ala Arg Thr Lys Arg Gly Val Ser Cys Tyr Gly Arg Tyr Met Pro Arg
435 440 445
Met Ile Ala Ile Pro Pro Gly Met Glu Phe Ser His Ile Val Pro His
450 455 460
Asp Val Asp Leu Asp Gly Asp Glu Ala Asn Glu Val Gly Ser Gly Ser
465 470 475 480

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Pro Asp Pro Pro Ile Trp Ala Asp Ile Met Arg Phe Phe Ser Asn Pro
                485                 490                 495
Arg Lys Pro Met Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn
            500                 505                 510
Ile Thr Thr Leu Val Lys Ala Phe Gly Glu His Pro Gly Leu Arg Asn
        515                 520                 525
Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Asp Val Ile Asp Glu
    530                 535                 540
Met Ser Ser Thr Asn Gly Ala Val Leu Thr Ser Val Leu Lys Leu Ile
545                 550                 555                 560
Asp Lys Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
                565                 570                 575
Gln Ser Glu Val Pro Asp Ile Tyr Arg Leu Ala Ala Arg Thr Lys Gly
            580                 585                 590
Val Phe Ile Asn Cys Ala Tyr Ile Glu Pro Phe Gly Leu Thr Leu Ile
        595                 600                 605
Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Gln Asn Gly Gly
    610                 615                 620
Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Ile Leu Val Asp Pro
625                 630                 635                 640
His Asn Gln Asn Asp Ile Ala Glu Ala Leu Tyr Lys Leu Val Ser Asp
                645                 650                 655
Lys His Leu Trp Ala Gln Cys Arg Gln Asn Gly Leu Asp Asn Ile His
            660                 665                 670
Arg Phe Ser Trp Pro Glu His Cys Lys Asn Tyr Leu Ser Arg Val Gly
        675                 680                 685
Thr Val Lys Pro Arg His Pro Arg Trp Gln Arg Ser Asp Asp Ala Thr
    690                 695                 700
Glu Val Ser Glu Ser Asp Ser Pro Gly Asp Ser Leu Arg Asp Val His
705                 710                 715                 720
Asp Ile Ser Leu Asn Leu Lys Leu Ser Leu Asp Ser Glu Lys Ala Gly
                725                 730                 735
Thr Lys Ile Asn Thr Glu Arg Asn Ser Thr Asn Ala Arg Arg Asn Leu
            740                 745                 750
Glu Asp Ala Val Leu Lys Phe Ser Asn Ala Val Ser Glu Gly Thr Lys
        755                 760                 765
Asp Glu Ser Asp Glu Asn Ala Glu Ala Thr Thr Gly Ser Ile Asn Gly
    770                 775                 780
His Leu Tyr Gly Glu Lys His Ile Val Val Ile Ala Val Asp Ser Val
785                 790                 795                 800
Gln Asn Ala Asp Leu Val Gln Ile Ile Lys Asn Leu Phe Glu Ala Ser
                805                 810                 815
Arg Lys Glu Lys Ser Ser Gly Ala Val Gly Phe Val Leu Ser Thr Ser
            820                 825                 830
Arg Ala Ile Ser Glu Thr Leu Thr Phe Leu Thr Ser Gly Gly Ile Gln
        835                 840                 845
Thr Thr Glu Phe Asp Ala Phe Ile Cys Ser Ser Gly Ser Asp Leu Cys
    850                 855                 860
Tyr Pro Ser Ser Ser Ser Glu Asp Met Leu Ser Pro Thr Glu Leu Pro
865                 870                 875                 880
Phe Met Ile Asp Leu Asp Tyr His Ser Gln Ile Glu Tyr Arg Trp Gly
                885                 890                 895
Gly Glu Gly Leu Arg Lys Thr Leu Ile Arg Trp Ala Ala Glu Asn Asn
            900                 905                 910
Ser Gln Ser Gly Gln Glu Val Val Thr Glu Asp Glu Glu Cys Ser Ser
        915                 920                 925
Thr Tyr Cys Ile Ser Phe Lys Val Lys Asn Thr Glu Ala Val Pro Pro
    930                 935                 940
Val Lys Asp Leu Arg Lys Thr Met Arg Ile Gln Ala Leu Arg Cys His
945                 950                 955                 960
Val Leu Tyr Ser His Asp Gly Ser Lys Leu Asn Leu Ile Pro Leu Leu
                965                 970                 975
Ala Ser Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Ile Arg Trp Gly Val
            980                 985                 990
Glu Leu Ala Asn Met Thr Val Val Val Gly Glu Ser Gly Asp Thr Asp
        995                 1000                1005
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Tyr Glu Gly Leu Leu Gly Gly Val His Lys Thr Ile Ile Leu Lys Gly
    1010                1015                1020
Ser Phe Asn Ala Ala Pro Asn Gln Leu His Ala Ala Arg Ser Tyr Ser
1025                1030                1035                1040
Leu Glu Asp Val Ile Ser Phe Asp Lys Pro Gly Ile Ala Ser Val Glu
                1045                1050                1055
Gly Tyr Leu Pro Asp Ser Leu Lys Ser Ala Leu Gln Gln Phe Gly Val
            1060                1065                1070
Leu Asn


<210> 73
<211> 937
<212> PRT
<213> Lolium perenne

<400> 73
Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
 1               5                  10                  15
Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
            20                  25                  30
Glu Thr Ala Pro Ala Leu Ala Ala Glu Glu Ser Ser Ala Ala Tyr Asn
        35                  40                  45
Pro Thr Arg Tyr Phe Val Glu Glu Val Val Arg Ser Phe Asp Glu Gln
    50                  55                  60
Ala Leu His Lys Thr Trp Thr Lys Val Val Ala Met Arg Asn Ser Gln
65                  70                  75                  80
Glu Arg Ser Asn Arg Leu Glu Asn Leu Cys Trp Arg Ile Trp Asn Val
                85                  90                  95
Ser Arg Gln Lys Lys Gln Val Glu Trp Asp Tyr Thr Lys Glu Val Ala
            100                 105                 110
Arg Arg Lys Leu Glu Gln Glu Leu Gly Ser Arg Glu Ala Ala Glu Asp
        115                 120                 125
Leu Ser Glu Leu Ser Glu Gly Glu Lys Asp Thr Thr Thr Ala Lys Pro
    130                 135                 140
Asp Ala Ala Ala Ala Gln Pro Ser Ala Asp Asp Gly Glu His Gln Gln
145                 150                 155                 160
Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
                165                 170                 175
Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
            180                 185                 190
Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
        195                 200                 205
Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
    210                 215                 220
Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
225                 230                 235                 240
Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
                245                 250                 255
Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Asp Asp Asp
            260                 265                 270
Gly Glu Gln Ala Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
        275                 280                 285
Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
    290                 295                 300
Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
305                 310                 315                 320
Leu Gly Glu Gln Leu Gln Pro Pro Pro Ser Pro Ala Asp Gly Ala Val
                325                 330                 335
Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His Tyr Ala Asp Ala
            340                 345                 350
Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn Val Pro Met Val
        355                 360                 365
Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu Gln Leu Leu Lys
    370                 375                 380
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Leu Gly Arg Met Pro Gly Pro Glu Ile Gln Gly Thr Tyr Lys Ile Ala
385                 390                 395                 400
Arg Arg Ile Glu Ala Glu Glu Thr Gly Leu Asp Thr Ala Glu Met Val
                405                 410                 415
Val Thr Ser Thr Lys Gln Glu Ile Glu Glu Gln Trp Gly Leu Tyr Asp
            420                 425                 430
Gly Phe Asp Leu Met Val Glu Arg Lys Leu Arg Val Arg Gln Arg Arg
        435                 440                 445
Gly Val Ser Ser Leu Gly Arg Tyr Met Pro Arg Met Ala Val Ile Pro
    450                 455                 460
Pro Gly Met Asp Phe Ser Phe Val Glu Thr Gln Asp Thr Ala Asp Gly
465                 470                 475                 480
Thr Gly Arg Ser Gln Met Leu Ile Ala Pro Asp Lys Ala Lys Lys Ala
                485                 490                 495
Leu Pro Pro Ile Trp Ser Asp Val Leu Arg Phe Phe Thr Asn Pro His
            500                 505                 510
Lys Pro Met Ile Leu Ala Leu Ser Arg Pro Asp Pro Lys Lys Asn Val
        515                 520                 525
Thr Thr Leu Leu Lys Ala Tyr Gly Glu Ser Arg Gln Leu Arg Glu Leu
    530                 535                 540
Ala Asn Leu Thr Leu Ile Leu Gly Asn Arg Asp Asp Ile Glu Asp Met
545                 550                 555                 560
Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val Leu Lys Leu Ile Asp
                565                 570                 575
Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys Gln
            580                 585                 590
Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly Val
        595                 600                 605
Phe Ile Asn Pro Ala Leu Val Glu Pro Phe Gly Leu Thr Ile Ile Glu
    610                 615                 620
Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr Lys Asn Gly Gly Pro
625                 630                 635                 640
Val Asp Ile Leu Lys Ala Leu His Asn Gly Leu Leu Val Asp Pro His
                645                 650                 655
Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser Leu Leu Ala Glu Lys
            660                 665                 670
Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu Arg Asn Ile His Arg
        675                 680                 685
Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu Ser His Val Ser Thr
    690                 695                 700
Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu Arg Val Pro Leu Ala
705                 710                 715                 720
Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp Ser Leu Ser Asp Ser
                725                 730                 735
Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp Ala Ser Ser Asp Leu
            740                 745                 750
Asn Ala Ala Asp Ser Ala Ala Ala Ile Met Asp Ala Leu Arg Arg Arg
        755                 760                 765
Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala Arg Ala Leu Gly Phe
    770                 775                 780
Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val Ala Val Asp Cys Tyr
785                 790                 795                 800
Gly Asp Asp Gly Lys Pro Asp Val Glu Gln Leu Lys Lys Ala Ile Asp
                805                 810                 815
Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala Lys Gln Gly Tyr Val
            820                 825                 830
Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala Glu Ala Ile Lys Ala
        835                 840                 845
Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu Ile Cys Ser Ser Gly
    850                 855                 860
Ala Glu Leu Cys Tyr Pro Trp Lys Lys Leu Val Ala Asp Glu Glu Tyr
865                 870                 875                 880
Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp His Val Lys Ser Ala
                885                 890                 895
Val Pro Arg Leu Gly Ser Met Glu Glu Ile Ala Leu Ala Ile Asp Arg
            900                 905                 910
```

Pro Ala Ser Ser Val His Cys His Ala Tyr Ala Ala Thr Asp Ala Ser
915 920 925
Lys Val Ser Ile Thr Glu His Tyr Leu
930 935

<210> 74
<211> 808
<212> PRT
<213> Lolium perenne

<400> 74
Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
1 5 10 15
Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
20 25 30
Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
35 40 45
Glu Phe Glu Ala Leu Phe Glu Ala Asp Lys Glu Arg Tyr Ala Pro Phe
50 55 60
Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
65 70 75 80
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
85 90 95
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
100 105 110
Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
115 120 125
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
130 135 140
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
145 150 155 160
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
165 170 175
Asn Phe Leu Lys Ala His Asn His Gln Gly Thr Thr Met Met Leu Asn
180 185 190
Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
195 200 205
Glu Glu Tyr Leu Thr Ser Ile Pro Glu Asp Thr Pro Ser Ser Glu Phe
210 215 220
Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
225 230 235 240
Ala Lys Arg Val Gln Asp Thr Ile His Leu Leu Leu Asp Leu Leu Glu
245 250 255
Ala Pro Asp Pro Ala Ser Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
260 265 270
Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
275 280 285
Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
290 295 300
Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
305 310 315 320
Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
325 330 335
Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
340 345 350
Gly Thr Glu His Thr Asp Ile Leu Arg Val Pro Phe Arg Thr Glu Lys
355 360 365
Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
370 375 380
Glu Thr Tyr Thr Glu Asp Val Ala Asn Glu Leu Met Arg Glu Met Gln
385 390 395 400
Thr Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
405 410 415
Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
420 425 430

His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
435 440 445
Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
450 455 460
Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
465 470 475 480
Ile Ala Gly Ser Lys Asp Ser Val Gly Gln Tyr Glu Ser His Ile Ala
485 490 495
Phe Thr Leu Pro Asp Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
500 505 510
Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Thr Val Tyr
515 520 525
Phe Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
530 535 540
Ile Glu Glu Leu Leu Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
545 550 555 560
Val Leu Lys Asp Lys Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
565 570 575
Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Phe Gly Lys Asn
580 585 590
Ala His Leu Lys Asp Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
595 600 605
Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
610 615 620
Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Glu Gly His Ile Arg Trp Ile
625 630 635 640
Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
645 650 655
Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
660 665 670
Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
675 680 685
Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asn Gly Val Ser Gly
690 695 700
Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
705 710 715 720
Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
725 730 735
Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
740 745 750
Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
755 760 765
Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
770 775 780
Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Ala Val Pro Leu Ala
785 790 795 800
Val Asp Gly Glu Asn Thr Asp Asn
805

<210> 75
<211> 808
<212> PRT
<213> Festuca arundinacea

<400> 75
Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
1 5 10 15
Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
20 25 30
Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
35 40 45
Glu Phe Glu Ala Leu Phe Glu Ser Asp Lys Glu Arg Tyr Ala Pro Phe
50 55 60
Gln Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
65 70 75 80

```
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
                85                  90                  95
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
            100                 105                 110
Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
        115                 120                 125
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
    130                 135                 140
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
145                 150                 155                 160
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
                165                 170                 175
Asn Phe Leu Lys Ala His Asn His Lys Gly Thr Thr Met Met Leu Asn
            180                 185                 190
Asp Arg Ile Thr Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
        195                 200                 205
Glu Glu Tyr Leu Thr Ser Ile Leu Glu Asp Thr Pro Ser Phe Glu Phe
    210                 215                 220
Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
225                 230                 235                 240
Ala Lys Arg Val Gln Asp Thr Ile His Leu Leu Leu Asp Leu Leu Glu
                245                 250                 255
Ala Pro Asp Pro Ala Ser Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
            260                 265                 270
Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
        275                 280                 285
Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
    290                 295                 300
Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
305                 310                 315                 320
Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
                325                 330                 335
Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
            340                 345                 350
Gly Thr Glu His Thr Asp Ile Leu Arg Val Pro Phe Arg Thr Glu Lys
        355                 360                 365
Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
    370                 375                 380
Glu Thr Tyr Thr Glu Asp Val Ala Asn Glu Leu Met Arg Glu Met Gln
385                 390                 395                 400
Thr Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
                405                 410                 415
Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
            420                 425                 430
His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
        435                 440                 445
Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
    450                 455                 460
Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
465                 470                 475                 480
Ile Ala Gly Ser Lys Asp Ser Val Gly Gln Tyr Glu Ser His Ile Ala
                485                 490                 495
Phe Thr Leu Pro Asp Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
            500                 505                 510
Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Ser Val Tyr
        515                 520                 525
Phe Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
    530                 535                 540
Ile Glu Glu Leu Leu Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
545                 550                 555                 560
Val Leu Lys Asp Lys Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
                565                 570                 575
Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Phe Gly Lys Asn
            580                 585                 590
Ala His Leu Lys Asp Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
        595                 600                 605
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```
Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
    610                 615                 620
Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Lys Gly His Ile Arg Trp Ile
625                 630                 635                 640
Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
                645                 650                 655
Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
            660                 665                 670
Gly Leu Thr Val Ile Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
        675                 680                 685
Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asp Gly Val Ser Gly
    690                 695                 700
Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
705                 710                 715                 720
Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
                725                 730                 735
Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
            740                 745                 750
Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
        755                 760                 765
Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
    770                 775                 780
Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Ala Val Pro Leu Ala
785                 790                 795                 800
Val Asp Gly Glu Asn Thr Asp Ser
                805

&lt;210&gt; 76
&lt;211&gt; 814
&lt;212&gt; PRT
&lt;213&gt; Lolium perenne

&lt;400&gt; 76
Met Gly Glu Ala Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val
 1               5                  10                  15
Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
            20                  25                  30
Ala Val Phe Thr Arg Leu Val Asn Leu Gly Lys Gly Met Leu Gln Pro
        35                  40                  45
His Gln Ile Ile Ala Glu Tyr Asn Thr Ala Ile Pro Glu Ala Glu Arg
    50                  55                  60
Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
65                  70                  75                  80
Glu Ala Ile Val Ile Ser Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
                85                  90                  95
Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
            100                 105                 110
Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
        115                 120                 125
Glu Gly Ser Asn Lys Asp Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
    130                 135                 140
Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn Gly
145                 150                 155                 160
Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp Lys
                165                 170                 175
Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr Lys
            180                 185                 190
Gly Met Pro Met Met Met Asn Asp Arg Val Arg Ser Leu Ser Ala Leu
        195                 200                 205
Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Gly Leu Pro Ala
    210                 215                 220
Asp Thr Pro Tyr Ser Asp Phe His His Arg Phe Gln Glu Leu Gly Leu
225                 230                 235                 240
Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Leu His
                245                 250                 255
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Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu Lys
            260                 265                 270
Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
        275                 280                 285
His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr Gly
    290                 295                 300
Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn Glu
305                 310                 315                 320
Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile
                325                 330                 335
Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys Gly
            340                 345                 350
Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu Arg
        355                 360                 365
Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser Arg
    370                 375                 380
Phe Glu Val Trp Pro Tyr Leu Glu Thr Phe Thr Asp Asp Val Ala His
385                 390                 395                 400
Glu Ile Ser Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly Asn
                405                 410                 415
Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met Gly
            420                 425                 430
Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
        435                 440                 445
Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe Ser
    450                 455                 460
Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe Ile
465                 470                 475                 480
Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val Gly
                485                 490                 495
Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Met Tyr Arg Val
            500                 505                 510
Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
        515                 520                 525
Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Ser Glu Ser Gln Arg Arg
    530                 535                 540
Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Asp Val
545                 550                 555                 560
Asp Asn Asp Glu His Ser Cys Leu Lys Asp Arg Asn Lys Pro Ile Ile
                565                 570                 575
Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val
            580                 585                 590
Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn Leu Val
        595                 600                 605
Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu Glu Gln
    610                 615                 620
Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn Leu Asn
625                 630                 635                 640
Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn Ala
                645                 650                 655
Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro
            660                 665                 670
Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Thr Cys
        675                 680                 685
Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu Ile Ile
    690                 695                 700
Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly Asp Lys
705                 710                 715                 720
Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Gly Asp His
                725                 730                 735
Ser His Trp Thr Lys Ile Ser Leu Gly Gly Leu Gln Arg Ile Glu Glu
            740                 745                 750
Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly
        755                 760                 765
Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr
    770                 775                 780
```

Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr Met Ala
785 790 795 800
Ser Thr Val Pro Leu Ala Val Glu Gly Glu Pro Ser Ser Lys
805 810

<210> 77
<211> 816
<212> PRT
<213> Festuca arundinacea

<400> 77
Met Gly Glu Ser Ala Gly Glu Arg Ala Leu Ser Arg Leu His Ser Val
1 5 10 15
Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Thr Asn Glu Leu Val
20 25 30
Ala Val Phe Ser Arg Leu Val Asn His Gly Lys Gly Met Leu Gln Pro
35 40 45
His Gln Ile Thr Ala Glu Tyr Asn Ala Ala Ile Pro Glu Ala Glu Arg
50 55 60
Glu Lys Leu Lys Asp Thr Ala Phe Glu Asp Leu Leu Arg Gly Ala Gln
65 70 75 80
Glu Ala Ile Val Ile Pro Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
85 90 95
Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Gly Val
100 105 110
Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
115 120 125
Asn Glu Ser Thr Asp Asn Asn Phe Val Leu Glu Leu Asp Phe Gly Pro
130 135 140
Phe Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn
145 150 155 160
Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp
165 170 175
Lys Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr
180 185 190
Lys Gly Met Thr Met Met Leu Asn Asp Arg Ile Arg Ser Leu Ser Ala
195 200 205
Leu Gln Asp Ala Leu Arg Lys Ala Glu Lys His Leu Ser Gly Leu Pro
210 215 220
Ala Asp Thr Pro Tyr Ser Glu Phe His His Arg Phe Gln Glu Leu Gly
225 230 235 240
Leu Glu Lys Gly Trp Gly Asp Cys Thr Gln Arg Ala His Glu Thr Ile
245 250 255
His Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu
260 265 270
Lys Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser
275 280 285
Pro His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr
290 295 300
Gly Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn
305 310 315 320
Glu Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Lys
325 330 335
Ile Leu Ile Val Thr Arg Leu Leu Pro Asp Ala His Gly Thr Thr Cys
340 345 350
Gly Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu
355 360 365
Arg Val Pro Phe Lys Thr Glu Asp Gly Ile Val Arg Lys Trp Ile Ser
370 375 380
Arg Phe Glu Val Trp Pro Tyr Leu Glu Ala Tyr Thr Asp Asp Val Ala
385 390 395 400
His Glu Ile Ala Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly
405 410 415
Asn Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Leu
420 425 430

```
Gly Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr
        435                 440                 445
Pro Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe
    450                 455                 460
Ser Cys Gln Phe Thr Ala Asp Leu Ile Ala Met Asn His Ala Asp Phe
465                 470                 475                 480
Ile Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val
                485                 490                 495
Gly Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg
            500                 505                 510
Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser
        515                 520                 525
Pro Gly Ala Asp Met Thr Ile Tyr Phe Pro Tyr Thr Glu Gln Gln Lys
    530                 535                 540
Arg Leu Thr Ser Leu His Ala Glu Ile Glu Glu Leu Leu Phe Ser Asp
545                 550                 555                 560
Val Glu Asn Ser Glu His Lys Phe Val Leu Lys Asp Lys Asn Lys Pro
                565                 570                 575
Ile Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Met Thr Gly
            580                 585                 590
Leu Val Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn
        595                 600                 605
Leu Val Val Val Cys Gly Asp His Gly Lys Glu Ser Lys Asp Lys Glu
    610                 615                 620
Glu Gln Ala Glu Phe Lys Arg Met Phe Asp Leu Ile Glu Gln Tyr Asn
625                 630                 635                 640
Leu Ser Ser His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg
                645                 650                 655
Asn Gly Glu Leu Tyr Arg Tyr Ile Cys Asp Met Lys Gly Ala Phe Val
            660                 665                 670
Gln Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met
        675                 680                 685
Thr Cys Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu
    690                 695                 700
Ile Ile Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Asn
705                 710                 715                 720
Asp Lys Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Glu
                725                 730                 735
Asp Pro Ser His Trp Asn Lys Ile Ser Gln Gly Gly Leu Gln Arg Ile
            740                 745                 750
Glu Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu
        755                 760                 765
Ser Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Asp Arg Arg
    770                 775                 780
Glu Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Lys
785                 790                 795                 800
Met Ala Thr Thr Val Pro Leu Ala Ile Glu Gly Glu Thr Thr Gly Lys
                805                 810                 815
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<210> 78
<211> 478
<212> PRT
<213> Festuca arundinacea

<400> 78
Trp Ile Ile Leu Glu Pro Ala Ile Glu Pro Asp Thr Pro Gly Asp Ile
1               5                   10                  15
Lys Gly Cys Trp Ser Ala Ser Ala Thr Val Ile Ser Gly Ser Gln Pro
            20                  25                  30
Val Ile Met Tyr Thr Gly Gly Asp Val Glu Asn His Gln Val Gln Asn
        35                  40                  45
Ile Ala Leu Pro Lys Asn Arg Ser Asp Pro Tyr Leu Ile Glu Trp Thr
    50                  55                  60
Lys Ala Cys Asn Asn Pro Val Leu Gln Pro Val Gly Pro Gly Met Asn
65                  70                  75                  80
```

Pro Gly Glu Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro Asp Gly
85 90 95
Leu Trp Arg Ile Ser Ile Gly Ala Glu Val Asn Gly Tyr Ser Ala Ala
100 105 110
Leu Leu Tyr Lys Ser Glu Asp Phe Leu Asn Trp Ser Arg Val Asp His
115 120 125
Pro Leu Tyr Ser Ser Ser Ala Ser Thr Met Trp Glu Cys Leu Asp Phe
130 135 140
Phe Ala Val Leu Pro Gly Ser Asn Gly Gly Leu Asp Leu Ser Ala Ala
145 150 155 160
Ile Pro Lys Gly Ala Lys His Val Leu Lys Val Ser Val Asp Gln Cys
165 170 175
Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Glu His Asp Ala Phe Val
180 185 190
Pro Asp Thr Ile Leu Asp Asp Arg Trp Leu Leu Pro Arg Ile Asp Tyr
195 200 205
Gly Asn Tyr Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Asn Arg Arg
210 215 220
Arg Ile Ile Trp Gly Trp Thr Asn Glu Ser Asp Ser Ser Ser Asp Asp
225 230 235 240
Val Ala Lys Gly Trp Ala Gly Ile Tyr Ala Ile Pro Arg Thr Ile Trp
245 250 255
Leu Asp Arg Asp Gly Lys Gln Leu Leu Gln Trp Pro Val Glu Glu Ile
260 265 270
Glu Ser Leu Arg Arg Asn Glu Ile Asn Tyr Gln Gly Leu Asp Leu Glu
275 280 285
Lys Gly Asp Leu Tyr Glu Ile Lys Gly Val Asp Thr Leu Gln Ala Asp
290 295 300
Val Glu Ile Asp Phe Glu Leu Thr Ser Ile Asp Asp Ala Asp Ser Phe
305 310 315 320
Asp Pro Ser Trp Leu Leu Asp Pro Glu Lys His Cys Arg Glu Ala Gly
325 330 335
Ala Ser Val His Gly Gly Ile Gly Pro Phe Gly Leu Val Ile Leu Ala
340 345 350
Thr Gly Asp Met Glu Glu His Thr Val Val His Phe Arg Val Tyr Lys
355 360 365
Ser Gln Lys Glu Tyr Met Ile Leu Met Cys Ser Asp Ile Arg Arg Ser
370 375 380
Ser Leu Arg Gln Gly Leu Tyr Ala Pro Ala Tyr Gly Gly Phe Phe Glu
385 390 395 400
Phe Asp Leu Glu Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu Ile Asp
405 410 415
Arg Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys Ile Ile
420 425 430
Ala Arg Val Tyr Pro Val Ala Ile Val Asp Asp Gly Ser Ala His Met
435 440 445
Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Ile Arg
450 455 460
Ala Trp Ser Met Met Thr Ala Gln Val Asn Leu Lys Lys Gly
465 470 475

<210> 79
<211> 583
<212> PRT
<213> Lolium perenne

<400> 79
Met Gly Asn Pro Lys Trp Val Leu Ala Pro Trp Ala Val Leu Leu Leu
1 5 10 15
Leu Gln Leu Ala Ser Ala Ser His His Ala Arg Leu Ser Leu Glu Thr
20 25 30
Ser Ala Ala Ser Pro Ser Val Pro Ala Ser Ile Val Ser Pro Leu Leu
35 40 45
Arg Thr Gly Tyr His Phe Gln Pro Pro Met Asn Trp Ile Asn Asp Pro
50 55 60

Asn Gly Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr
65 70 75 80
Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Ile Trp Ala His Ser Val
85 90 95
Ser Arg Asp Leu Ile Asn Trp Ile Ala Leu Glu Pro Ala Ile Ser Pro
100 105 110
Thr Ile Pro Thr Asp Gln Tyr Gly Val Trp Ser Gly Ser Thr Thr Ile
115 120 125
Leu His Asp Gly Thr Pro Ala Ile Leu Tyr Thr Gly Ile Asp Arg Pro
130 135 140
Ser Val Asn Tyr Gln Ile Gln Asn Ile Ala Leu Pro Lys Asn Ala Ser
145 150 155 160
Asp Pro Leu Leu Arg Glu Trp Tyr Lys Pro Gly Tyr Asn Pro Ile Ala
165 170 175
Val Pro Val Glu Gly Ile Asn Ala Thr Gln Phe Arg Asp Pro Thr Thr
180 185 190
Ala Trp Phe Ala Gly Arg His Trp Arg Met Leu Val Gly Gly Leu Arg
195 200 205
Pro Gly Thr Leu Arg Gly Glu Ala Ile Leu Tyr Arg Ser Arg Asp Phe
210 215 220
Lys His Trp Val Arg Ala Lys His Pro Leu His Ser Ala Leu Thr Gly
225 230 235 240
Met Trp Glu Cys Pro Asp Phe Phe Pro Val Gly Lys Ala Gly Val Glu
245 250 255
Lys Gly Leu Asp Thr Ser Glu Tyr Gly Ala Ala Ala Gly Val Glu Lys
260 265 270
His Val Leu Lys Asn Ser Leu Asp Leu Thr Arg Tyr Asp Tyr Tyr Thr
275 280 285
Ile Gly Thr Tyr Asp Asn Val Lys Glu Arg Tyr Val Pro Asp Asn Pro
290 295 300
Thr Gly Asp Val Tyr Gln Arg Leu Gln Tyr Asp Tyr Gly Asn Phe Tyr
305 310 315 320
Ala Ser Lys Thr Phe Phe Asp Pro Val Lys Gln Arg Arg Ile Leu Leu
325 330 335
Gly Trp Ala Asn Glu Ser Asp Ser Val Ala His Asp Lys Ala Lys Gly
340 345 350
Trp Ala Gly Ile Gln Ala Ile Pro Arg Lys Ile Trp Leu Asp Pro Ser
355 360 365
Gly Lys Gln Leu Val Gln Trp Pro Val Glu Glu Leu Glu Lys Leu Arg
370 375 380
Gly Lys Pro Val Asn Val Gly Asp Lys Val Val Lys Pro Gly Gln His
385 390 395 400
Phe Glu Val Thr Gly Leu Gln Ser Tyr Gln Ser Asp Val Glu Val Ser
405 410 415
Phe Glu Val Ser Ser Leu Asp Lys Ala Glu Pro Phe Asp Pro Ala Tyr
420 425 430
Ser Asn Asp Ala Gln Lys Leu Cys Gly Ile Lys Gly Ala Asp Val Lys
435 440 445
Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ser Ser Ala Asp Leu
450 455 460
Ala Glu Lys Thr Ala Val Phe Phe Arg Val Phe Lys Asp Gly Tyr Gly
465 470 475 480
Lys Pro Ile Val Leu Met Cys Ser Asp Pro Thr Lys Ser Ser Leu Thr
485 490 495
Pro Asp Leu Tyr Lys Pro Thr Phe Ala Gly Phe Val Asp Thr Asp Ile
500 505 510
Ser Ser Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp Arg Ser Val Val
515 520 525
Glu Ser Phe Gly Ala Gly Gly Lys Thr Cys Ile Leu Ser Arg Val Tyr
530 535 540
Pro Ser Met Ala Leu Gly Lys Asp Ala His Leu His Val Phe Asn Asn
545 550 555 560
Gly Glu Thr Asp Ile Lys Val Ser Lys Leu Thr Ala Trp Glu Met Lys
565 570 575
Arg Pro Leu Met Asn Gly Ala
580

<210> 80
<211> 390
<212> PRT
<213> Lolium perenne

<400> 80
Gly Val Gly Ser Leu Leu Val Tyr Arg Ser Ala Asp Phe Leu Arg Trp
1 5 10 15
Gln Arg Asn Ala Ala Pro Leu His Ala Ser Ser Arg Asp Val Pro Val
20 25 30
Leu Glu Cys Pro Asp Leu Phe Pro Val Ala Ala Ala Ala Gln Gly Ala
35 40 45
Thr Glu Gly Leu Glu Thr Ser Ala Pro Ser Gly Ala Gly Val Arg His
50 55 60
Val Leu Lys Leu Thr Asp Phe Ala Lys Glu Asp His Tyr Met Val Gly
65 70 75 80
Phe Tyr Asp Asp Val Ala Asp Thr Phe Val Pro Ala Glu Pro Glu Arg
85 90 95
Gly Asp Asp Pro Asp Asn Trp Arg Arg Leu Asp His Gly His Leu Tyr
100 105 110
Ala Ser Lys Ser Phe Tyr Asp Ala Arg Asn Lys Arg Arg Ile Leu Trp
115 120 125
Ala Trp Val Asp Glu Thr Asp Gly Gly Gly Val Ala Arg Gly Trp Ala
130 135 140
Gly Ile Gln Ala Phe Pro Arg Ala Met Trp Leu Asp Ala Asp Gly Lys
145 150 155 160
Arg Leu Val Gln Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg Lys
165 170 175
Arg Val Gly Leu Arg Trp Ala Thr Asp Val Glu Ala Gly Gly Arg Lys
180 185 190
Glu Ile Ala Gly Ile Val Ser Ser Gln Ala Asp Val Glu Val Val Phe
195 200 205
Glu Ile Pro Asn Leu Glu Glu Ala Glu Thr Leu Asp Pro Glu Trp Val
210 215 220
Leu Asp Pro Lys Gly Leu Cys Ala Ala Lys Gly Ala Ser Val His Gly
225 230 235 240
Gly Val Gly Pro Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Glu
245 250 255
Glu His Thr Ala Val Phe Phe Arg Val Phe Lys His Asp Gly Lys Tyr
260 265 270
Lys Val Leu Met Cys Thr Asp Leu Thr Lys Ser Ser Thr Lys Ala Gly
275 280 285
Ala His Lys Pro Ser Tyr Gly Ala Phe Leu Asp Val Asp Val Glu Lys
290 295 300
Asp Lys Phe Ile Ser Leu Arg Thr Leu Ile Asp His Thr Val Val Glu
305 310 315 320
Ser Phe Gly Asp Gly Gly Arg Thr Cys Met Thr Ala Arg Val Tyr Pro
325 330 335
Glu His Ala Ala Met Gly Ser Thr His Leu Tyr Val Phe Asn Asn Gly
340 345 350
Thr Gly Ala Val Lys Val Ser Lys Leu Glu Ala Trp Glu Leu Ala Thr
355 360 365
Ala Ala Val Asn Gly Gly Ser Leu Ala Pro Val Val Val Lys Ala Ser
370 375 380
Asp Pro Lys Glu Ala Leu
385 390

<210> 81
<211> 597
<212> PRT
<213> Festuca arundinacea

<400> 81
Met Ala Gly Leu Arg Leu Ala Ala Cys Ala Ala Val Ala Val Leu Leu
1 5 10 15

```
Cys Leu Leu Leu Ser Ser Ser Ala Ala Leu Arg Trp Leu Ser Asp Pro
            20                  25                  30
Ala Pro Glu Ser Ala Ala Ala Gly Val Ser His Asp Ser Tyr Arg Thr
        35                  40                  45
Ala Tyr His Phe Gln Pro Thr Glu Asn Trp Gln Asn Asp Pro Asn Gly
    50                  55                  60
Pro Met Tyr Tyr Lys Gly Val Tyr His Phe Phe Tyr Gln Tyr Asn Pro
65                  70                  75                  80
Tyr Arg Ala Thr Trp Gly Asn Gly Asn Leu Ser Trp Gly His Ser Val
                85                  90                  95
Ser Val Asp Leu Val Asn Trp Ser Ala Leu Glu Asn Ala Met Asp Pro
            100                 105                 110
Asp Ser Ser Phe Asp Ile Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile
        115                 120                 125
Leu Pro Asp Gly Thr Pro Val Phe Leu Tyr Thr Gly Ile Asp Ala Asp
    130                 135                 140
Asn Asn Gln Val Gln Asn Val Ala Phe Pro Lys Asn Ala Ser Asp Pro
145                 150                 155                 160
Leu Leu Arg Glu Trp Val Lys Pro Ser Tyr Asn Pro Val Ile Ala Leu
                165                 170                 175
Pro Asp Asp Val Val His Asp Asn Phe Arg Asp Pro Ser Thr Ala Trp
            180                 185                 190
Leu Gly Arg Asp Gly Leu Trp Arg Val Ala Val Ser Ala Gly Leu Lys
        195                 200                 205
Asp Gly Thr Gly Thr Thr Leu Val Tyr Arg Ser Lys Asp Phe Arg Gln
    210                 215                 220
Trp Glu Arg Asn Ala Glu Pro Leu Tyr Ser Ser Ser Asp Ala Gly Met
225                 230                 235                 240
Val Glu Cys Pro Asp Leu Phe Pro Leu Ala Glu Pro Gly Asp Gln His
                245                 250                 255
Gly Leu Asp Tyr Thr Pro Ser Asn Gly Ala Ala Val Ser Tyr Val Leu
            260                 265                 270
Lys Gln Ser Val Met Asp Thr Leu Ser Asp Tyr Tyr Val Leu Gly Arg
        275                 280                 285
Tyr Asp Asp Ala Ala Asp Thr Phe Ser Pro Val Glu Ala Asp Asn Asp
    290                 295                 300
Cys Arg Thr Trp Gln Arg Phe Asp Tyr Gly His Val Tyr Ala Ser Lys
305                 310                 315                 320
Ser Phe Tyr Asp Ala Gly Lys Lys Arg Arg Val Leu Trp Ser Trp Ala
                325                 330                 335
Asn Glu Ser Asp Pro Glu Ala Asp Tyr Leu Ala Arg Gly Trp Ala Gly
            340                 345                 350
Val Gln Ala Val Pro Arg Arg Ile Trp Leu Asp Ser Lys Gly Lys Gln
        355                 360                 365
Leu Leu Gln Trp Pro Ile Glu Glu Ile Glu Thr Leu Arg Lys Thr Arg
    370                 375                 380
Val Gly Leu Leu Gly Ala Glu Met Asn Ala Gly Gly Met Asn Glu Ile
385                 390                 395                 400
Ile Gly Val Ala Gly Ala Gln Ala Asp Val Glu Val Val Phe Glu Val
                405                 410                 415
Pro Ser Leu Glu Gly Ala Glu Asn Leu Asp Pro Asn Gln Leu Leu Asp
            420                 425                 430
Pro Gln Arg Leu Cys Gly Glu Lys Gly Ala Ser Val Leu Gly Gly Val
        435                 440                 445
Gly Pro Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Gln Glu His
    450                 455                 460
Thr Ser Val Phe Phe Arg Val Phe Arg His Glu Gly Lys Tyr Lys Val
465                 470                 475                 480
Leu Met Cys Thr Asp Leu Arg Arg Ser Thr Thr Arg Ala Asp Val Tyr
                485                 490                 495
Lys Pro Pro Tyr Gly Gly Phe Val Asp Ile Asp Ile Glu Lys Glu Arg
            500                 505                 510
Ser Ile Ser Leu Arg Thr Leu Val Asp His Ser Val Val Glu Ser Tyr
        515                 520                 525
Gly Gly Gly Gly Arg Thr Val Ile Thr Ala Arg Val Tyr Pro Glu His
    530                 535                 540
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```
Ala Ala Thr Thr Asn Ser Arg Leu Phe Met Phe Asn Asn Gly Thr Gly
545                 550                 555                 560
Ala Val Lys Val Ser Lys Leu Asp Ala Trp Glu Leu Ala Pro Ala Lys
                565                 570                 575
Val Asn Val Pro Gly Asp Gly Leu Ile Thr Ala Gly Ser Ser Met His
            580                 585                 590
Leu Arg Glu Ala Tyr
        595

<210> 82
<211> 399
<212> PRT
<213> Festuca arundinacea

<400> 82
Leu Asn Ser Thr Glu Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro
 1               5                  10                  15
Asp Gly Leu Trp Arg Ile Ala Ile Gly Ala Glu Leu Asn Gly Tyr Gly
            20                  25                  30
Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu Asn Trp Thr Arg Val
        35                  40                  45
Asp His Pro Leu Tyr Ser Asp Asn Ala Pro Ser Met Trp Glu Cys Pro
    50                  55                  60
Asp Phe Phe Ala Val Leu Pro Gly Asn Asn Gly Gly Leu Asp Leu Ser
65                  70                  75                  80
Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu Lys Met Ser Val Asp
                85                  90                  95
Tyr Ser Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Arg Asp Ala
            100                 105                 110
Phe Val Pro Asp Val Val Leu Asp Asp Arg Arg Leu Trp Leu Arg Ile
        115                 120                 125
Asp Tyr Gly Thr Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Arg
    130                 135                 140
Gly Arg Arg Val Ile Trp Gly Trp Ser Asn Glu Thr Asp Ser Val Ser
145                 150                 155                 160
Asp Asp Gly Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg Ser
                165                 170                 175
Ile Trp Leu Asp Ser Asp Gly Lys Gln Leu Leu Gln Trp Pro Ile Asp
            180                 185                 190
Glu Ile Glu Ser Leu Arg Arg Asp Glu Ile Asn His Gln Gly Leu Glu
        195                 200                 205
Leu Lys Asn Gly Asp Leu Phe Glu Ile Lys Gly Ile Asp Thr Leu Gln
    210                 215                 220
Ala Asp Ile Glu Val Asp Phe Glu Leu Thr Ser Ile Asp Ser Ala Asp
225                 230                 235                 240
Pro Phe Asp Pro Ser Trp Leu Leu Asp Val Glu Arg His Cys Arg Glu
                245                 250                 255
Ala Gly Ala Ser Val Gln Gly Gly Ile Gly Pro Phe Gly Leu Val Val
            260                 265                 270
Leu Ala Ser Asp Asn Met Glu Glu His Ile Ala Val His Phe Arg Val
        275                 280                 285
Tyr Lys Ser Gln Lys Ser His Met Ile Leu Met Cys Ser Asp Leu Arg
    290                 295                 300
Arg Ser Ser Leu Arg Ser Gly Leu Tyr Thr Pro Ala Tyr Gly Gly Phe
305                 310                 315                 320
Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu
                325                 330                 335
Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys
            340                 345                 350
Ile Thr Ala Arg Ile Tyr Pro Val Ala Leu Val Asp Gly Arg Val His
        355                 360                 365
Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Leu
    370                 375                 380
Gly Ala Trp Ser Met Met Thr Ala Gln Val Asn Val Asn Lys Gly
385                 390                 395
```

<210> 83
<211> 583
<212> PRT
<213> Festuca arundinacea

<400> 83
Met Gly Asn Pro Lys Trp Ile Phe Ala Pro Trp Ala Val Leu Leu Leu
1 5 10 15
Phe Leu Leu Gln Leu Ala Cys Ala Ser His His Thr Arg Arg Ser Leu
20 25 30
Glu Thr Glu Ala Ala Ser Pro Ser Val Pro Ala Ser Ile Val Ser Pro
35 40 45
Leu Leu Arg Thr Gly Tyr His Phe Gln Pro Pro Met Asn Trp Ile Asn
50 55 60
Asp Pro Asn Gly Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr
65 70 75 80
Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Ile Trp Ala His
85 90 95
Ser Val Ser Arg Asp Leu Ile Asn Trp Ile Ala Leu Glu Pro Ala Ile
100 105 110
Thr Pro Ser Ile Pro Thr Asp Lys Tyr Gly Val Trp Ser Gly Ser Thr
115 120 125
Thr Ile Leu His Asp Gly Thr Pro Ala Ile Leu Tyr Thr Gly Ile Asp
130 135 140
Arg Pro Ser Ile Asn Tyr Gln Ile Gln Asn Ile Ala Leu Pro Lys Asn
145 150 155 160
Ala Ser Asp Pro Leu Leu Arg Glu Trp Tyr Lys Pro Gly Tyr Asn Pro
165 170 175
Ile Ala Val Pro Val Ala Gly Met Asn Ala Thr Gln Phe Arg Asp Pro
180 185 190
Thr Thr Ala Trp Phe Ala Gly Arg His Trp Arg Met Leu Val Gly Gly
195 200 205
Leu Arg Pro Gly Thr Leu Arg Gly Glu Ala Ile Leu Tyr Arg Ser Leu
210 215 220
Asp Phe Lys Asn Trp Thr Arg Ala His His Pro Leu His Ser Ala Leu
225 230 235 240
Thr Gly Met Trp Glu Cys Pro Asp Phe Phe Pro Val Gly Glu Ala Gly
245 250 255
Val Glu Lys Gly Leu Asp Thr Ser Glu His Gly Glu Gly Val Glu Lys
260 265 270
His Val Leu Lys Asn Ser Leu Asp Leu Thr Arg Tyr Asp Tyr Tyr Thr
275 280 285
Val Gly Thr Tyr Asp Asn Val Lys Glu Arg Tyr Val Pro Asp Asn Pro
290 295 300
Thr Gly Asp Val Tyr Arg Arg Leu Gln Tyr Asp Tyr Gly Asn Phe Tyr
305 310 315 320
Ala Ser Lys Thr Phe Phe Asp Pro Val Lys Gln Arg Arg Ile Leu Leu
325 330 335
Gly Trp Ala Asn Glu Ser Asp Ser Val Ala His Asp Lys Ala Lys Gly
340 345 350
Trp Ala Gly Ile Gln Ala Ile Pro Arg Lys Ile Trp Leu Asp Pro Ser
355 360 365
Gly Lys Gln Leu Val Gln Trp Pro Val Glu Glu Leu Glu Lys Leu Arg
370 375 380
Gly Lys Pro Val Thr Val Gly Asp Lys Val Val Lys Pro Gly Gln His
385 390 395 400
Phe Glu Val Thr Gly Leu Gln Ser Tyr Gln Ser Asp Val Glu Val Ser
405 410 415
Phe Glu Val Ser Ser Leu Asp Lys Ala Glu Pro Phe Asp Pro Ala Tyr
420 425 430
Ser Asn Asp Ala Gln Lys Leu Cys Gly Ile Lys Gly Ala Asp Ala Asn
435 440 445
Gly Gly Val Gly Pro Phe Gly Leu Val Val Leu Ala Ser Ala Asp Leu
450 455 460
Ala Glu Lys Thr Ala Val Phe Phe Arg Val Phe Lys Asp Gly Tyr Gly
465 470 475 480

```
Lys Pro Ile Val Leu Met Cys Ser Asp Pro Thr Lys Ser Ser Leu Thr
                485                 490                 495
Pro Asp Leu Tyr Lys Pro Thr Phe Ala Gly Phe Val Asp Thr Asp Ile
            500                 505                 510
Ser Ser Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp Arg Ser Val Val
        515                 520                 525
Glu Ser Phe Gly Ala Gly Gly Lys Thr Cys Ile Leu Ser Arg Val Tyr
    530                 535                 540
Pro Ser Met Ala Leu Gly Lys Asn Ala His Leu His Val Phe Asn Asn
545                 550                 555                 560
Gly Glu Thr Asp Ile Lys Val Ser Lys Leu Thr Val Trp Glu Met Lys
                565                 570                 575
Arg Pro Leu Met Asn Gly Ala
            580
```

<210> 84
<211> 346
<212> PRT
<213> Lolium perenne

<400> 84

```
Met Tyr Tyr Asn Gly Ile Tyr His Glu Phe Tyr Gln Tyr Asn Pro Asn
 1               5                  10                  15
Gly Ser Leu Trp Gly Asn Ile Ile Trp Gly His Ser Val Ser Thr Asp
            20                  25                  30
Leu Ile Asn Trp Ile Pro Val Glu Pro Ala Ile Glu Arg Asp Ile Pro
        35                  40                  45
Ser Asp Ile Asn Gly Cys Trp Thr Gly Ser Ala Thr Ile Ile Ser Gly
    50                  55                  60
Asp Gln Pro Ile Ile Ile Tyr Thr Gly Ala Asp Lys Glu Asn Arg Gln
65                  70                  75                  80
Leu Gln Asn Ile Val Leu Pro Lys Asn Lys Ser Asp Pro Tyr Leu Arg
                85                  90                  95
Glu Trp Thr Lys Ala Gly Asn Asn Pro Val Ile Gln Pro Val Gly Pro
            100                 105                 110
Gly Leu Asn Ala Ser Gln Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly
        115                 120                 125
Pro Asp Gly Leu Trp Arg Ile Ala Val Gly Ala Glu Leu Asn Gly Tyr
    130                 135                 140
Gly Ala Ala Leu Leu Tyr Lys Ser Gln Asp Phe Leu Asn Trp Thr Arg
145                 150                 155                 160
Val Asp His Pro Leu Tyr Ser Ser Asn Ala Ser Ser Met Trp Glu Cys
                165                 170                 175
Pro Asp Phe Phe Ala Val Leu Pro Gly Asn Ser Gly Gly Leu Asp Leu
            180                 185                 190
Ser Ala Glu Ile Pro Asn Gly Ala Lys His Val Leu Lys Met Ser Leu
        195                 200                 205
Asp Ser Cys Asp Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Ser Asp
    210                 215                 220
Thr Phe Met Pro Asp Ser Val Leu Asp Asp Arg Arg Leu Trp Ser Arg
225                 230                 235                 240
Ile Asp His Gly Asn Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys
                245                 250                 255
Lys Gly Arg Arg Ile Ile Trp Gly Trp Thr Asn Glu Thr Asp Ser Ser
            260                 265                 270
Ser Asp Asp Val Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg
        275                 280                 285
Thr Ile Trp Leu Asp Ser Tyr Gly Lys Gln Leu Leu Gln Trp Pro Ile
    290                 295                 300
Glu Glu Ile Glu Ser Leu Arg Arg Asn Glu Ile Ser His Gln Gly Leu
305                 310                 315                 320
Glu Leu Lys Lys Gly Asp Leu Phe Glu Ile Lys Gly Thr Asp Thr Ser
                325                 330                 335
Gln Val Val His Val Phe Leu Gly Lys Leu
            340                 345
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<210> 85
<211> 581
<212> PRT
<213> Festuca arundinacea

<400> 85
Met Ala Gly Leu Arg Leu Ala Ala Val Ala Phe His Leu Cys Leu Leu
1 5 10 15
Leu Ser Pro Ser Ser Ser Leu Arg Arg Leu Tyr His Glu Asp Asp Glu
20 25 30
Ala Glu Ser Thr Pro Gly His Gly Gly Ser Arg Thr Ala Tyr His Phe
35 40 45
Gln Pro Ala Lys Asn Trp Gln Asn Asp Pro Asn Gly Pro Met Tyr His
50 55 60
Asn Gly Leu Tyr His Leu Phe Tyr Gln Tyr Asn Pro Arg Gly Ala Thr
65 70 75 80
Trp Gly Asn Gly Asn Leu Ser Trp Gly His Ser Val Ser Val Asp Leu
85 90 95
Val Asn Trp Ala Ala Leu Asp Thr Ala Leu Asp Pro Asp Ser Pro Phe
100 105 110
Asp Ala Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile Leu Pro Asp Gly
115 120 125
Gln Pro Ala Ile Leu Tyr Thr Gly Ile Asp Ala Ala Gly Asn Gln Val
130 135 140
Gln Asn Val Ala Phe Pro Lys Lys Ala Ser Asp Pro Leu Leu Arg Glu
145 150 155 160
Trp Val Lys Pro Asp Tyr Asn Pro Val Ile Pro Leu Pro Lys Asp Val
165 170 175
Val His Asp Ser Phe Arg Asp Pro Ser Thr Ala Trp Arg Gly Arg Asp
180 185 190
Gly Leu Trp Arg Val Ala Ile Ala Ala Lys Val Asn Val Thr Val Thr
195 200 205
Val Gly Ser Thr Leu Ile Tyr Arg Ser Lys Asp Phe Arg Arg Trp Glu
210 215 220
Arg Asn Ala Ala Pro Leu Tyr Glu Ser Leu Ala Ala Gly Met Val Glu
225 230 235 240
Cys Pro Asp Leu Phe Pro Val Ala Lys Pro Gly Ala Gln Asn Gly Leu
245 250 255
Asp Tyr Ala Pro Ser Ser Arg Ala Ala Arg His Val Leu Lys Leu Ser
260 265 270
Val Val Ala Thr Leu Gln Asp Tyr Tyr Val Val Gly Leu Tyr Asp Asp
275 280 285
Thr Ala Asp Thr Phe Asn Ala Ala Ala Gly Ala Asp Asn Asp Trp Arg
290 295 300
Thr Trp Arg Arg Ile Asp Tyr Gly His Val Tyr Ala Ser Lys Ser Phe
305 310 315 320
Phe Asp Ala Arg Lys Asn Arg Arg Val Leu Trp Cys Trp Ala Asn Glu
325 330 335
Ser Asp Thr Glu Ala Asp Tyr Ile Ala Arg Gly Trp Ser Gly Val Gln
340 345 350
Thr Val Pro Arg Lys Ile Trp Leu Asp Ile Asp Gly Lys Gln Leu Leu
355 360 365
Gln Trp Pro Ile Lys Glu Ile Glu Thr Leu Arg Lys Lys Arg Val Gly
370 375 380
Leu Leu Gly Thr Glu Met Asn Ser Gly Gly Leu Asn Glu Ile Ile Gly
385 390 395 400
Val Ala Gly Ser Gln Ala Asp Val Glu Val Val Phe Lys Ile Pro Thr
405 410 415
Leu Glu Gly Ala Glu Asn Ile Glu Pro Asn Glu Leu Leu Asp Pro Gln
420 425 430
Lys Leu Cys Gly Asn Asn Gly Ala Ser Met Arg Gly Ser Ile Gly Pro
435 440 445
Phe Gly Leu Leu Leu Leu Ala Ser Gly Asp Leu Leu Glu His Thr Ser
450 455 460
Val Phe Phe Arg Val Phe Lys His Gly Ala Lys Tyr Lys Val Leu Met
465 470 475 480

```
Cys Thr Asp Leu Thr Arg Ser Thr Thr Arg Ser Asp Val Tyr Lys Pro
                485                 490                 495
Ser Tyr Gly Gly Phe Val Asp Met Asp Ile Asp Lys Thr Lys Ser Ile
            500                 505                 510
Ser Leu Arg Thr Leu Ile Asp His Ser Val Val Glu Ser Phe Gly Gly
        515                 520                 525
Gly Gly Arg Thr Cys Ile Thr Ala Arg Val Tyr Pro Glu His Ala Glu
    530                 535                 540
Met Ser Asn Ser His Ile Tyr Met Phe Asn Asn Gly Thr Gly Ala Val
545                 550                 555                 560
Lys Val Ala Lys Leu Glu Ala Trp Glu Leu Ala Thr Ala Asn Val Asn
                565                 570                 575
Val Ala Gly His Gly
            580

<210> 86
<211> 588
<212> PRT
<213> Lolium perenne

<400> 86
Met Gly Val Arg Leu Gly Arg Val Ala Trp Ala Cys Pro Ala Val Leu
 1               5                  10                  15
Val Leu Leu Leu Gln Leu Ala Gly Ala Ser His Val Val Tyr Glu Thr
            20                  25                  30
Ser Leu Leu Glu Thr Glu Ala Ala Ala Ala Thr Val Pro Ala Ser Ile
        35                  40                  45
Phe Glu Leu Ser Thr Gly Tyr His Phe Arg Pro Gln Lys Asn Trp Ile
    50                  55                  60
Asn Asp Pro Asn Ala Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe
65                  70                  75                  80
Phe Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Val Trp Ala
                85                  90                  95
His Ser Val Ser Arg Asp Leu Ile Asn Trp Val Ala Leu Glu Thr Ala
            100                 105                 110
Leu Ala Pro Ser Ile Asp Ala Asp Lys Tyr Gly Cys Trp Ser Gly Ser
        115                 120                 125
Ala Thr Ile Met Pro Asp Gly Thr Pro Val Ile Met Tyr Thr Gly Val
    130                 135                 140
Ser Arg Pro Asp Val Asn Tyr Glu Val Gln Asn Val Ala Phe Pro Lys
145                 150                 155                 160
Asn Ser Ser Asp Pro Leu Leu Arg Glu Trp Val Lys Pro Ala His Asn
                165                 170                 175
Pro Val Ile Val Pro Glu Gly Gly Ile Asn Ala Thr Gln Phe Arg Asp
            180                 185                 190
Pro Thr Thr Ala Trp Tyr Ala Asp Gly His Trp Arg Ile Leu Val Gly
        195                 200                 205
Ala Leu Ser Gly Ala Ser Arg Gly Val Ala Tyr Val Tyr Arg Ser Arg
    210                 215                 220
Asp Phe Arg Arg Trp Thr Arg Val Arg Lys Pro Leu His Ser Ala Pro
225                 230                 235                 240
Thr Gly Met Trp Glu Cys Pro Asp Phe Tyr Pro Val Thr Val Asp Gly
                245                 250                 255
Lys Glu Ser Gly Val Asp Thr Ser Val Val Ser Ser Ser Arg Val Lys
            260                 265                 270
His Val Leu Lys Asn Ser Leu Asp Leu Arg Arg Tyr Asp Tyr Tyr Thr
        275                 280                 285
Val Gly Thr Tyr Asp Arg Leu Lys Glu Arg Tyr Val Pro Asp Asn Pro
    290                 295                 300
Ala Gly Asp Lys His His Leu Arg Tyr Asp Tyr Gly Asn Phe Tyr Ala
305                 310                 315                 320
Ser Lys Thr Phe Tyr Asp Pro Ser Lys Arg Arg Arg Ile Leu Trp Gly
                325                 330                 335
Trp Ala Asn Glu Ser Asp Thr Ala Val Asp Asp Val Ala Lys Gly Trp
            340                 345                 350
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Ala Gly Ile Gln Ala Ile Pro Arg Lys Val Trp Leu Asp Pro Ser Gly
355 360 365
Arg Gln Leu Met Gln Trp Pro Val Glu Glu Val Lys Ala Leu Arg Gly
370 375 380
Lys Lys Pro Val Ser Leu Lys Asp Arg Met Val Lys Arg Gly Glu His
385 390 395 400
Val Glu Val Thr Gly Leu Gln Thr Ala Gln Ala Asp Val Glu Val Ser
405 410 415
Phe Glu Val Pro Ser Leu Glu Gly Ala Glu Ala Leu Asp Pro Ala Leu
420 425 430
Ala Asn Asp Ala Gln Lys Leu Cys Gly Val Lys Gly Ala Asp Val Glu
435 440 445
Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ala Ser Ser Lys Leu
450 455 460
Glu Glu Arg Thr Ala Val Phe Phe Arg Val Phe Lys Ala Ala Gly Asn
465 470 475 480
Val Asn Ser Thr Lys Pro Leu Val Leu Met Cys Ser Asp Pro Thr Lys
485 490 495
Ser Ser Leu Asn Lys Asn Leu Tyr His Pro Thr Phe Ala Gly Phe Val
500 505 510
Asp Ile Asp Met Ala Lys Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp
515 520 525
Gln Ser Val Val Glu Ser Phe Gly Ala Gly Gly Arg Thr Cys Ile Leu
530 535 540
Ser Arg Val Tyr Pro Ser Leu Ala Ile Gly Arg Asn Ala His Leu His
545 550 555 560
Val Phe Asn Asn Gly Lys Ala Asp Ile Lys Val Ser Arg Leu Thr Ala
565 570 575
Trp Glu Met Lys Lys Pro Ala Leu Met Asn Gly Ala
580 585

<210> 87
<211> 668
<212> PRT
<213> Lolium perenne

<400> 87
Met Glu Ala Arg Asp Gly Val Ser Met Pro Tyr Ser Tyr Ala Ala Leu
1 5 10 15
Pro Glu Asp Ala Glu Ala Ala Val Val Gly Arg Gly Arg Arg Thr Gly
20 25 30
Pro Leu Phe Ala Ala Leu Leu Leu Thr Leu Val Ala Ala Leu Leu Ala
35 40 45
Val Ala Ala Leu Ala Gly Val Arg Leu Val Gly Glu Leu Pro Ala Gly
50 55 60
Gly Val Val Met Pro Asn His Pro Met Glu Val Met Asp Val Ser Gly
65 70 75 80
Ser Arg Gly Pro Glu Ser Gly Val Ser Glu Lys Thr Ser Gly Ala Ala
85 90 95
Ser Glu Ser Gly Gly Met Leu Gly Ala Asp Ala Gly Ser Asn Ala Phe
100 105 110
Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe
115 120 125
Gln Pro Glu Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr
130 135 140
Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Glu Gly Ala Ile
145 150 155 160
Trp Gly Asn Lys Ile Ala Trp Gly His Ala Val Ser Arg Asp Met Leu
165 170 175
Arg Trp Arg His Leu Pro Ile Ala Met Phe Pro Asp Gln Trp Tyr Asp
180 185 190
Ile Asn Gly Ala Trp Ser Gly Ser Ala Thr Val Leu Pro Asp Gly Arg
195 200 205
Ile Val Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln Val Gln
210 215 220

```
Cys Leu Ala Phe Pro Ser Asp Pro Ser Asp Pro Leu Leu Thr Asn Trp
225                 230                 235                 240
Thr Lys Tyr Glu Gly Asn Pro Val Leu Tyr Pro Pro Pro His Val Gly
                245                 250                 255
Glu Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Tyr Asp Gly Ser Asp
            260                 265                 270
Gly Met Trp Arg Ile Val Ile Gly Ser Lys Asp Asn Arg Arg Ala Gly
        275                 280                 285
Met Ala Leu Thr Tyr Lys Thr Lys Asn Phe His Asp Phe Glu Leu Val
    290                 295                 300
Pro Gly Val Leu His Arg Val Pro Ala Thr Gly Met Trp Glu Cys Ile
305                 310                 315                 320
Asp Leu Tyr Pro Val Gly Gly Ala Arg Gly Ile Asp Met Thr Glu Ala
                325                 330                 335
Val Ala Ala Ala Ser Asn Ser Gly Gly Gly Glu Val Leu His Val Met
            340                 345                 350
Lys Glu Ser Ser Asp Asp Asp Arg His Asp Tyr Tyr Ala Leu Gly Arg
        355                 360                 365
Tyr Asp Ala Ala Thr Asn Lys Trp Thr Pro Leu Asp Ala Asp Ala Asp
    370                 375                 380
Val Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Lys
385                 390                 395                 400
Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp Gly Trp Val
                405                 410                 415
Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly Trp Ala Ser
            420                 425                 430
Leu Gln Ser Ile Pro Arg Thr Val Val Leu Asp Thr Lys Thr Gly Ser
        435                 440                 445
Asn Leu Ile Gln Trp Pro Val Val Glu Val Glu Thr Leu Arg Thr Asn
    450                 455                 460
Ser Thr Asn Leu Gly Ser Ile Ile Val Glu His Gly Ser Val Phe Pro
465                 470                 475                 480
Leu Ser Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser Phe Arg
                485                 490                 495
Leu Asp Pro Leu Asp Val Ala Ala Ala Lys Glu Ala Asp Val Gly Tyr
            500                 505                 510
Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly Arg Gly Ala Leu Gly Pro
        515                 520                 525
Phe Gly Leu Leu Val Leu Ala Asp Ala Arg Arg His Gly Gly Asp Thr
    530                 535                 540
Glu Gln Thr Ala Val Tyr Phe Tyr Val Ala Arg Gly Leu Asp Gly Asn
545                 550                 555                 560
Leu Arg Thr His Phe Cys His Asp Glu Ser Arg Ser Ser Arg Ala Asn
                565                 570                 575
Asp Ile Val Lys Arg Val Val Gly Asn Ile Val Pro Val Leu Asp Gly
            580                 585                 590
Lys Ala Leu Ser Val Arg Val Leu Val Ala His Ser Ile Val Glu Ser
        595                 600                 605
Phe Ala Gln Gly Gly Arg Ser Val Val Thr Ser Arg Val Tyr Pro Thr
    610                 615                 620
Glu Ala Ile Tyr Ala Asn Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr
625                 630                 635                 640
Gly Ala Arg Val Pro Ala Thr Ser Leu Val Val His Lys Met Asp Pro
                645                 650                 655
Ser Tyr Asn Gln Asn Gln Ala Glu Met Ala Ser Leu
            660                 665
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<210> 88
<211> 473
<212> PRT
<213> Lolium perenne

<400> 88

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Val His Trp Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr
1               5                   10                  15
```

Asp Ile Asn Gly Val Trp Thr Gly Ser Ala Thr Val Phe Pro Asp Gly
20 25 30
Thr Leu Asn Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln Ala
35 40 45
Gln Cys Leu Ala Val Pro Glu Asp Pro Asn Asp Ser Leu Leu Arg Asn
50 55 60
Trp Thr Lys His Glu Ala Asn Pro Val Leu Leu Pro Pro Pro Gly Ile
65 70 75 80
Gly Asp Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Phe Asp Glu Ser
85 90 95
Asp Gln Thr Trp Arg Thr Val Ile Gly Ser Lys Asp Asn Asn Gly His
100 105 110
Ala Gly Ile Ala Met Val Tyr Lys Thr Lys Asp Phe Leu Asn Tyr Glu
115 120 125
Leu Ile Pro Gly Tyr Leu His Arg Val Asp Gly Thr Gly Met Trp Glu
130 135 140
Cys Ile Asp Phe Tyr Pro Val Gly Gly Lys Asn Gly Ser Glu Glu Leu
145 150 155 160
Tyr Val Ile Lys Glu Ser Ser Asp Asp Asp Arg His Asp Trp Tyr Thr
165 170 175
Leu Gly Lys Tyr Asp Ala Ala Ala Asn Thr Phe Thr Ala Ala Asp Pro
180 185 190
Glu Asn Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr
195 200 205
Ala Ser Lys Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp
210 215 220
Gly Trp Ile Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly
225 230 235 240
Trp Ala Ser Leu Met Ser Ile Pro Arg Thr Val Glu Leu Asp Glu Lys
245 250 255
Thr Trp Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Ile Glu Thr Leu
260 265 270
Arg Ile Lys Ser Thr Asp Leu Gly Gly Ile Thr Ile Asp His Gly Ser
275 280 285
Val Tyr Pro Leu Pro Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala
290 295 300
Ser Phe Arg Leu Asp Ala Ala Thr Val Ala Ala Leu Asn Glu Ala Asp
305 310 315 320
Val Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ser Thr His Arg Gly Ala
325 330 335
Leu Gly Pro Phe Gly Ile Leu Val Leu Ala Asp Gly Lys Ala Glu Gln
340 345 350
Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Leu Asp Gly Ala Leu Glu
355 360 365
Thr His Phe Cys His Asp Glu Ser Arg Ser Thr Leu Ala Lys Asp Val
370 375 380
Val Lys Arg Val Val Gly Tyr Thr Val Pro Val Leu Asp Gly Glu Ala
385 390 395 400
Phe Ser Val Arg Val Leu Val Asp His Ser Ile Val Glu Ser Phe Ala
405 410 415
Met Gly Gly Arg Ser Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu Ser
420 425 430
Ile Tyr Gly Ala Ala Gly Ala Tyr Leu Phe Asn Asn Ala Thr Gly Gly
435 440 445
Ser Val Thr Val Glu Lys Leu Val Val His Glu Met Asp Ser Ser Tyr
450 455 460
Asn Gln Ile Phe Met Ala Asp Asp Leu
465 470

<210> 89
<211> 539
<212> PRT
<213> Lolium perenne

<400> 89
Ile Phe Arg Ser Arg Leu Pro Asp Ile Asp Ile Pro Thr His Met Pro
1 5 10 15
Leu His Asp Tyr Cys Phe Ala Thr Ala Ala Ser Ala Pro Asp Ala Pro
20 25 30
Cys Leu Ile Thr Ala Ala Thr Gly Arg Thr Tyr Thr Phe Ala Glu Thr
35 40 45
His Leu Leu Cys Arg Lys Ala Ala Ala Ala Leu His Gly Leu Gly Val
50 55 60
Arg His Gly Asp Arg Ile Met Val Leu Leu Gln Asn Ser Val Glu Phe
65 70 75 80
Ala Leu Ala Phe Phe Gly Ala Ser Met Leu Gly Ala Val Ser Thr Ala
85 90 95
Ala Asn Pro Phe Cys Thr Pro Gln Glu Ile His Lys Gln Leu Val Ala
100 105 110
Ser Gly Ala Lys Leu Val Val Thr Gln Ser Ala Tyr Val Asp Lys Leu
115 120 125
Arg His Glu Ala Phe Pro Arg Ile Gly Glu Ala Leu Thr Val Ile Thr
130 135 140
Ile Asp Asp Asp Gly Thr Pro Asp Gly Cys Gln Pro Phe Trp Gly Leu
145 150 155 160
Val Ser Ala Ala Asp Glu Asn Ser Val Pro Glu Ser Pro Ile Ser Pro
165 170 175
Asp Asp Ala Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro
180 185 190
Lys Gly Val Val Leu Thr His Gly Gly Leu Val Ser Ser Val Ala Gln
195 200 205
Gln Val Asp Gly Glu Asn Pro Asn Leu His Met Arg Ala Gly Glu Asp
210 215 220
Val Val Leu Cys Val Leu Pro Leu Phe His Ile Phe Ser Leu Asn Ser
225 230 235 240
Val Leu Leu Cys Ala Leu Arg Ala Gly Ala Ala Val Met Leu Met Pro
245 250 255
Arg Phe Glu Met Gly Ala Met Leu Glu Gly Ile Glu Arg Trp Arg Val
260 265 270
Thr Val Ala Ala Val Val Pro Pro Leu Val Leu Ala Leu Ala Lys Asn
275 280 285
Pro Gly Val Glu Lys His Asp Leu Ser Ser Ile Arg Ile Val Leu Ser
290 295 300
Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ala Leu Arg Gly Arg
305 310 315 320
Leu Pro Gln Ala Ile Phe Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly
325 330 335
Pro Val Leu Ser Met Cys Pro Ala Phe Ala Arg Glu Pro Thr Pro Ala
340 345 350
Lys Ser Gly Ser Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val
355 360 365
Val Asp Pro Asp Thr Gly Val Ser Leu Gly Arg Asn Leu Pro Gly Glu
370 375 380
Ile Cys Ile Arg Gly Pro Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro
385 390 395 400
Val Ala Thr Ala Ala Thr Ile Asp Val Glu Gly Trp Leu His Thr Gly
405 410 415
Asp Ile Gly Tyr Val Asp Asp Asp Asp Glu Val Phe Ile Val Asp Arg
420 425 430
Val Lys Glu Leu Ile Lys Phe Lys Gly Phe Gln Val Pro Pro Ala Glu
435 440 445
Leu Glu Ala Leu Leu Ile Ala His Pro Ser Ile Ala Asp Ala Ala Val
450 455 460
Val Pro Gln Lys Asp Asp Ala Ala Gly Glu Val Pro Val Ala Phe Val
465 470 475 480
Val Arg Ala Ala Asp Ser Asp Ile Ala Glu Glu Ala Ile Lys Glu Phe
485 490 495
Val Ser Lys Gln Val Val Phe Tyr Lys Arg Leu His Lys Val Tyr Phe
500 505 510

Thr His Ala Ile Pro Lys Ser Ala Ser Gly Lys Ile Leu Arg Lys Glu
515 520 525
Leu Arg Ala Lys Leu Ala Ala Pro Ala Thr Ala
530 535

<210> 90
<211> 559
<212> PRT
<213> Lolium perenne

<400> 90
Met Gly Ser Ile Ala Ala Asp Leu Ala Pro Glu Ala Pro Ala Glu Leu
1 5 10 15
Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Pro Thr His Leu Thr
20 25 30
Leu Gln Asp Tyr Cys Phe Glu Arg Leu Pro Glu Leu Ser Ala Arg Ala
35 40 45
Cys Leu Ile Asp Gly Ala Thr Gly Ala Ala Leu Thr Tyr Gly Glu Val
50 55 60
Asp Ala Leu Ser Arg Arg Cys Ala Ala Gly Leu Arg Arg Leu Gly Val
65 70 75 80
Arg Lys Gly Asp Val Val Met Ala Leu Leu Arg Asn Cys Pro Glu Phe
85 90 95
Ala Phe Val Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr Thr
100 105 110
Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Ala Ala
115 120 125
Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys Val
130 135 140
Arg Ala Phe Ala Ala Glu Arg Gly Ile Pro Val Val Ser Val Asp Glu
145 150 155 160
Ala Val Asp Asp Gly Cys Leu Pro Phe Ala Ala Thr Leu Leu Gly Glu
165 170 175
Glu Ser Gly Glu Arg Phe Val Asp Glu Ala Val Asp Pro Asp Asp Val
180 185 190
Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val
195 200 205
Met Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Gln Val Asp
210 215 220
Gly Glu Asn Pro Asn Leu His Phe Ser Ser Ser Asp Val Leu Leu Cys
225 230 235 240
Val Leu Pro Leu Phe His Ile Tyr Ser Leu Asn Ser Val Leu Leu Ala
245 250 255
Gly Leu Arg Ala Gly Cys Ala Ile Val Ile Met Arg Lys Phe Asp His
260 265 270
Gly Ala Leu Val Asp Leu Val Arg Ala His Gly Val Thr Val Ala Pro
275 280 285
Phe Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Ala Arg Val Thr
290 295 300
Ala Ala Asp Leu Ala Ser Ile Arg Leu Val Met Ser Gly Ala Ala Pro
305 310 315 320
Met Gly Lys Glu Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala
325 330 335
Val Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala
340 345 350
Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Glu Val Lys Ser Gly Ser
355 360 365
Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Ile Val Asp Pro Asp
370 375 380
Thr Gly Ala Ser Leu Gly Arg Asn Leu Pro Gly Glu Ile Cys Ile Arg
385 390 395 400
Gly Lys Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu Ala Thr Lys
405 410 415
Asn Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr
420 425 430

Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile
435 440 445
Ile Lys Tyr Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu Ala Leu
450 455 460
Leu Ile Thr His Pro Glu Ile Lys Asp Ala Ala Val Val Ser Met Gln
465 470 475 480
Asp Glu Leu Ala Gly Glu Val Pro Val Ala Phe Val Val Arg Thr Glu
485 490 495
Gly Ser Glu Ile Ser Glu Asn Glu Ile Lys Gln Phe Val Ala Lys Glu
500 505 510
Val Val Phe Tyr Lys Arg Ile Cys Lys Val Phe Phe Ala Asp Ser Ile
515 520 525
Pro Lys Ser Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys
530 535 540
Leu Ala Ala Gly Ile Pro Gly Ser Asp Thr Thr Gln Ser Lys Asn
545 550 555

<210> 91
<211> 559
<212> PRT
<213> Festuca arundinacea

<400> 91
Met Gly Ser Ile Ala Ala Asp Ala Pro Glu Ala Pro Pro Ala Glu Leu
1 5 10 15
Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Pro Thr His Leu Thr
20 25 30
Leu Gln Asp Tyr Cys Phe Gln Arg Leu Pro Glu His Ser Ala Arg Ala
35 40 45
Cys Leu Ile Asp Gly Ala Thr Gly Ala Ala Leu Thr Tyr Gly Glu Val
50 55 60
Asp Ala Leu Ser Arg Arg Cys Ala Ala Gly Leu Arg Arg Leu Gly Val
65 70 75 80
Arg Lys Gly Asp Val Val Met Ala Leu Leu Arg Asn Cys Pro Glu Phe
85 90 95
Ala Phe Val Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr Thr
100 105 110
Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Thr Ala
115 120 125
Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys Val
130 135 140
Arg Ala Phe Ala Ala Glu Arg Gly Ile Thr Val Val Ser Val Asp Glu
145 150 155 160
Gly Val Asp Asp Gly Cys Leu Pro Phe Gly Glu Thr Leu Leu Gly Glu
165 170 175
Asp Gly Gly Glu Arg Phe Val Asp Glu Ala Val Asp Pro Asp Asp Val
180 185 190
Val Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val
195 200 205
Met Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Gln Val Asp
210 215 220
Gly Glu Asn Pro Asn Leu His Phe Ser Ser Ser Asp Val Leu Leu Cys
225 230 235 240
Val Leu Pro Leu Phe His Ile Tyr Ser Leu Asn Ser Val Leu Leu Ala
245 250 255
Gly Leu Arg Ala Gly Cys Ala Ile Val Ile Met Arg Lys Phe Asp His
260 265 270
Gly Ala Leu Val Asp Leu Val Arg Ala His Gly Val Thr Val Ala Pro
275 280 285
Phe Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Ala Arg Val Thr
290 295 300
Ala Ala Asp Leu Ala Ser Ile Arg Leu Val Met Ser Gly Ala Ala Pro
305 310 315 320
Met Gly Lys Glu Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala
325 330 335

Val Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala
340 345 350
Met Cys Leu Ala Phe Ala Lys Glu Pro Phe Glu Val Lys Ser Gly Ser
355 360 365
Cys Gly Thr Val Val Arg Asn Ala Glu Leu Lys Ile Val Asp Pro Asp
370 375 380
Thr Gly Ala Ser Leu Gly Arg Asn Leu Pro Gly Glu Ile Cys Ile Arg
385 390 395 400
Gly Lys Gln Ile Met Lys Gly Tyr Leu Asn Asp Pro Glu Ala Thr Lys
405 410 415
Asn Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Tyr
420 425 430
Val Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile
435 440 445
Ile Lys Tyr Lys Gly Phe Gln Val Pro Pro Ala Glu Leu Glu Ala Leu
450 455 460
Leu Ile Thr His Pro Glu Ile Lys Asp Ala Ala Val Val Ser Met Gln
465 470 475 480
Asp Glu Leu Ala Gly Glu Val Pro Val Ala Phe Val Val Arg Thr Glu
485 490 495
Gly Ser Glu Ile Ser Glu Asn Glu Ile Lys Gln Phe Val Ala Lys Glu
500 505 510
Val Val Phe Tyr Lys Arg Ile Cys Lys Val Phe Phe Ala Asp Ser Ile
515 520 525
Pro Lys Ser Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Lys
530 535 540
Leu Ala Ala Gly Ile Pro Gly Ser Glu Thr Thr Gln Ser Lys Ser
545 550 555

<210> 92
<211> 557
<212> PRT
<213> Lolium perenne

<400> 92
Met Gly Ser Val Pro Glu Glu Ser Val Val Ser Val Ala Ala Ala Glu
1 5 10 15
Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
20 25 30
Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
35 40 45
Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
50 55 60
Val Asp Tyr Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
65 70 75 80
Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
85 90 95
Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
100 105 110
Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
115 120 125
Ala Ala Gly Ala Lys Leu Ile Val Thr Glu Ala Cys Ala Val Glu Lys
130 135 140
Val Leu Glu Phe Ala Ala Gly Arg Gly Leu Pro Val Val Thr Val Asp
145 150 155 160
Gly Arg Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
165 170 175
Glu Leu Pro Glu Ala Asp Glu Ala Gly Ile Leu Pro Asp Asp Val Val
180 185 190
Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
195 200 205
Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Val Asp Gly
210 215 220
Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
225 230 235 240

Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
245 250 255
Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly
260 265 270
Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
275 280 285
Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Gly Ala
290 295 300
Asp Asp Leu Ala Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
305 310 315 320
Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
325 330 335
Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
340 345 350
Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
355 360 365
Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
370 375 380
Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
385 390 395 400
Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
405 410 415
Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
420 425 430
Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
435 440 445
Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
450 455 460
Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
465 470 475 480
Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
485 490 495
Ser Glu Ile Thr Glu Asn Glu Ile Lys Gln Phe Val Ser Lys Glu Val
500 505 510
Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
515 520 525
Lys Asn Pro Ser Gly Lys Ile Val Arg Lys Asp Leu Arg Ala Arg Leu
530 535 540
Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
545 550 555

<210> 93
<211> 557
<212> PRT
<213> Festuca arundinacea

<400> 93
Met Gly Ser Val Pro Glu Glu Ser Val Val Ala Ala Ala Val Ala Glu
1 5 10 15
Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
20 25 30
Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
35 40 45
Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
50 55 60
Val Glu Ser Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
65 70 75 80
Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
85 90 95
Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
100 105 110
Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
115 120 125
Ala Ala Gly Ala Lys Val Ile Val Thr Glu Ala Cys Ala Val Glu Lys
130 135 140

Val Leu Glu Phe Ala Ala Glu Arg Gly Leu Pro Val Val Thr Val Asp
145 150 155 160
Gly Lys Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
165 170 175
Glu Leu Pro Glu Ala Glu Glu Ala Gly Ile Leu Pro Asp Asp Val Val
180 185 190
Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
195 200 205
Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Phe Asp Gly
210 215 220
Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
225 230 235 240
Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
245 250 255
Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly
260 265 270
Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
275 280 285
Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Thr Ala
290 295 300
Asp Asp Leu Thr Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
305 310 315 320
Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
325 330 335
Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
340 345 350
Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
355 360 365
Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
370 375 380
Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
385 390 395 400
Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
405 410 415
Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
420 425 430
Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
435 440 445
Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
450 455 460
Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
465 470 475 480
Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
485 490 495
Ser Glu Ile Thr Glu Asn Asp Ile Lys Gln Phe Val Ser Lys Glu Val
500 505 510
Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
515 520 525
Lys Asn Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Arg Leu
530 535 540
Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
545 550 555

<210> 94
<211> 501
<212> PRT
<213> Lolium perenne

<400> 94
Met Glu Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
1 5 10 15
Ala Val Leu Ala Ile Ala Val Ala Lys Leu Ala Gly Lys Arg Phe Arg
20 25 30
Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
35 40 45

Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Ile Ala Lys Arg
50 55 60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
65 70 75 80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
85 90 95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
100 105 110
Asn Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
115 120 125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
130 135 140
Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
145 150 155 160
Val Lys Ala Asp Pro Ala Phe Ala Thr Ala Gly Thr Val Ile Arg Arg
165 170 175
Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
180 185 190
Arg Arg Phe Glu Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
195 200 205
Met Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
210 215 220
Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Lys Tyr Leu Asn
225 230 235 240
Arg Cys Thr Asn Leu Thr Thr Lys Arg Met Lys Leu Phe Glu Asp His
245 250 255
Phe Val Ala Asp Arg Lys Lys Ala Leu Glu Gln Asn Gly Glu Ile Arg
260 265 270
Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
275 280 285
His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
290 295 300
Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
305 310 315 320
His Pro Asp Val Gln Ser Lys Leu Arg Asp Glu Met Thr Ala Val Leu
325 330 335
Gly Ala Asp Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
340 345 350
Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
355 360 365
Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
370 375 380
Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
385 390 395 400
Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
405 410 415
Phe Leu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
420 425 430
Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Val Leu
435 440 445
Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
450 455 460
Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
465 470 475 480
Pro Gly Gln Phe Ser Asn Gln Ile Leu Lys His Ala Thr Val Val Cys
485 490 495
Lys Pro Leu Glu Ala
500

<210> 95
<211> 505
<212> PRT
<213> Festuca arundinacea

<400> 95

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Met Asp Phe Val Phe Val Glu Lys Leu Leu Val Gly Leu Leu Ala Ser
 1               5                  10                  15
Val Val Val Ala Ile Val Val Ser Lys Ile Arg Gly Arg Lys Leu Arg
            20                  25                  30
Leu Pro Pro Gly Pro Ile Pro Val Pro Ile Phe Gly Asn Trp Leu Gln
        35                  40                  45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Ala Ala Met Ala Arg Lys
    50                  55                  60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
65                  70                  75                  80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
                85                  90                  95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
            100                 105                 110
Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
        115                 120                 125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Gln
    130                 135                 140
Gln Tyr Arg Ala Gly Trp Glu Ala Glu Ala Ala Phe Val Val Asp Asn
145                 150                 155                 160
Val Arg Ala Asp Pro Lys Ala Ala Thr Asp Gly Val Val Leu Arg Arg
                165                 170                 175
His Leu Gln Leu Met Met Tyr Asn Asn Met Tyr Arg Ile Met Phe Asp
            180                 185                 190
Arg Arg Phe Glu Ser Met Asp Asp Pro Leu Phe Leu Arg Leu Arg Ala
        195                 200                 205
Leu Asn Gly Glu Arg Ser Arg Leu Ala Gln Ser Phe Glu Tyr Asn Tyr
    210                 215                 220
Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Gly Tyr Leu Gly
225                 230                 235                 240
Leu Cys Glu Gln Val Lys Glu Thr Arg Leu Lys Leu Phe Lys Asp Tyr
                245                 250                 255
Phe Leu Asp Glu Arg Lys Lys Leu Ala Ser Thr Lys Ser Met Asp Thr
            260                 265                 270
Asn Gly Leu Lys Cys Ala Ile Asp His Ile Leu Glu Ala Gln Glu Lys
        275                 280                 285
Gly Glu Ile Asn Glu Asp Asn Val Leu Tyr Ile Ile Glu Asn Ile Asn
    290                 295                 300
Val Ala Ala Ile Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala
305                 310                 315                 320
Glu Leu Val Asn His Pro Glu Ile Gln Gln Lys Leu Arg Asp Glu Met
                325                 330                 335
Asp Ala Val Leu Gly Ala Gly His Gln Ile Thr Glu Pro Asp Thr His
            340                 345                 350
Lys Leu Pro Tyr Leu Gln Ala Val Ile Lys Glu Thr Leu Arg Leu Arg
        355                 360                 365
Met Ala Ile Pro Leu Leu Val Pro His Met Asn Leu His Asp Ala Lys
    370                 375                 380
Leu Ala Gly Tyr Asn Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala
385                 390                 395                 400
Trp Phe Leu Ala Asn Asn Pro Glu Gln Trp Lys Arg Pro Asp Glu Phe
                405                 410                 415
Arg Pro Glu Arg Phe Leu Glu Glu Glu Lys His Val Glu Ala Ser Gly
            420                 425                 430
Asn Asp Phe Arg Phe Leu Pro Phe Gly Val Gly Arg Arg Ser Cys Pro
        435                 440                 445
Gly Ile Ile Leu Ala Leu Pro Ile Leu Gly Ile Thr Ile Gly Arg Leu
    450                 455                 460
Val Gln Asn Phe Glu Leu Thr Thr Pro Pro Gly Val Asp Lys Leu Asp
465                 470                 475                 480
Thr Thr Glu Lys Gly Gly Gln Phe Ser Leu His Ile Leu Asn His Ser
                485                 490                 495
Thr Ile Val Ala Lys Pro Arg Val Phe
            500                 505
```

<210> 96
<211> 361
<212> PRT
<213> Lolium perenne

<400> 96
Met Gly Ile Val Asn Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
1 5 10 15
Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Thr Tyr Asn Leu Arg Arg
20 25 30
Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
35 40 45
His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Pro Lys Tyr
50 55 60
Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
65 70 75 80
Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
85 90 95
Ile Val Gly Cys Cys Arg Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
100 105 110
Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
115 120 125
Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ser Met Val Val Asp Gln
130 135 140
Lys Phe Val Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
145 150 155 160
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
165 170 175
Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly
180 185 190
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
195 200 205
Thr Val Ile Ser Ser Ser Asp Lys Lys Arg Ala Glu Ala Met Asp Asp
210 215 220
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
225 230 235 240
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
245 250 255
His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu
260 265 270
Val Leu Met Gly Val Ile Gly Glu Pro Leu Ser Phe Val Ser Pro Met
275 280 285
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
290 295 300
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Asp Lys Gly Leu Thr
305 310 315 320
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn Gln Ala Leu Glu
325 330 335
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
340 345 350
Gly Ser Asn Ile Asp Asp Thr Ala Ala
355 360

<210> 97
<211> 361
<212> PRT
<213> Festuca arundinacea

<400> 97
Met Gly Ser Val Asp Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
1 5 10 15
Arg Asp Thr Thr Gly His Leu Ser Pro Tyr Thr Tyr Thr Leu Arg Arg
20 25 30
Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
35 40 45

```
His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Ser Lys Tyr
    50                  55                  60
Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
65                  70                  75                  80
Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
                85                  90                  95
Ile Val Gly Cys Cys His Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
            100                 105                 110
Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
        115                 120                 125
Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ala Met Val Val Asp Gln
    130                 135                 140
Lys Phe Ala Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
145                 150                 155                 160
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
                165                 170                 175
Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly
            180                 185                 190
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
        195                 200                 205
Thr Val Ile Ser Ser Ser Asn Lys Lys Arg Ala Glu Ala Met Asp Asp
    210                 215                 220
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
225                 230                 235                 240
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
                245                 250                 255
His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu
            260                 265                 270
Val Leu Met Gly Val Ile Ala Glu Pro Leu Ser Phe Val Ser Pro Met
        275                 280                 285
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
    290                 295                 300
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Glu Lys Gly Leu Thr
305                 310                 315                 320
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn His Ala Leu Glu
                325                 330                 335
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
            340                 345                 350
Gly Ser Asn Ile Lys Asp Ala Asp Ala
        355                 360
```

<210> 98
<211> 265
<212> PRT
<213> Lolium perenne

<400> 98

```
Met Ala Thr Thr Ala Ala Asp Ala Thr Ala Thr Val Ala Lys Glu Gln
1               5                   10                  15
Thr Thr Thr Asn Gly Ala Ala Ser Gly Ala Glu Gln Val Thr Arg His
            20                  25                  30
Ser Glu Val Gly His Lys Ser Leu Leu Gln Ser Asp Ala Leu Tyr Gln
        35                  40                  45
Tyr Ile Leu Glu Thr Thr Val Tyr Pro Arg Glu His Glu Cys Met Lys
    50                  55                  60
Gln Leu Arg Glu Asp Thr Ala Asn His Pro Trp Asn Leu Met Thr Thr
65                  70                  75                  80
Ser Ala Asp Glu Gly Gln Phe Leu Asn Leu Leu Ile Lys Leu Ile Gly
                85                  90                  95
Ala Lys Lys Thr Met Glu Ile Gly Val Tyr Thr Gly Tyr Ser Leu Leu
            100                 105                 110
Ala Thr Ala Leu Ala Ile Pro Glu Asp Gly Thr Ile Leu Ala Met Asp
        115                 120                 125
Ile Asn Arg Glu Asn Tyr Glu Thr Ile Gly Lys Pro Cys Ile Glu Lys
    130                 135                 140
```

Ala Gly Val Ala His Lys Ile Asp Phe Arg Glu Gly Pro Ala Leu Pro
145 150 155 160
Val Leu Asp Glu Leu Leu Glu Asp Glu Ala Asn His Gly Thr Phe Asp
165 170 175
Phe Val Phe Val Asp Ala Asp Lys Asp Asn Tyr Leu Asn Tyr His Gln
180 185 190
Arg Leu Met Lys Leu Val Arg Val Gly Gly Leu Leu Gly Tyr Asp Asn
195 200 205
Thr Leu Trp Asn Gly Ser Val Val Leu Pro Ala Asp Ala Pro Met Arg
210 215 220
Lys Tyr Ile Arg Tyr Tyr Arg Asp Phe Val Leu Glu Leu Asn Lys Ala
225 230 235 240
Leu Ala Ala Asp Asp Arg Val Glu Ile Cys Gln Leu Pro Val Gly Asp
245 250 255
Gly Ile Thr Leu Cys Arg Arg Ala Lys
260 265

<210> 99
<211> 265
<212> PRT
<213> Festuca arundinacea

<400> 99
Met Ala Thr Thr Ala Ala Asp Ala Thr Ala Thr Val Pro Lys Glu Gln
1 5 10 15
Pro Ala Thr Asn Gly Ala Ala Ser Gly Ala Glu Gln Val Thr Arg His
20 25 30
Ser Glu Val Gly His Lys Ser Leu Leu Gln Ser Asp Ala Leu Tyr Gln
35 40 45
Tyr Ile Leu Glu Thr Thr Val Tyr Pro Arg Glu His Glu Cys Met Lys
50 55 60
Gln Leu Arg Glu Asp Thr Ala Asn His Pro Trp Asn Leu Met Thr Thr
65 70 75 80
Ser Ala Asp Glu Gly Gln Phe Leu Asn Leu Leu Ile Lys Leu Ile Gly
85 90 95
Ala Lys Lys Thr Met Glu Ile Gly Val Tyr Thr Gly Tyr Ser Leu Leu
100 105 110
Ala Thr Ala Leu Ala Ile Pro Glu Asp Gly Thr Ile Leu Ala Met Asp
115 120 125
Ile Asn Arg Glu Asn Tyr Glu Thr Ile Gly Lys Pro Cys Ile Glu Lys
130 135 140
Ala Gly Val Ala His Lys Ile Asp Phe Arg Glu Gly Pro Ala Leu Pro
145 150 155 160
Val Leu Asp Glu Leu Leu Glu Asp Glu Ala Asn His Gly Ser Phe Asp
165 170 175
Phe Val Phe Val Asp Ala Asp Lys Asp Asn Tyr Leu Asn Tyr His Gln
180 185 190
Arg Leu Met Lys Leu Val Arg Val Gly Gly Leu Ile Gly Tyr Asp Asn
195 200 205
Thr Leu Trp Asn Gly Ser Val Val Leu Pro Ala Asp Ala Pro Met Arg
210 215 220
Lys Tyr Ile Arg Tyr Tyr Arg Asp Phe Val Leu Glu Leu Asn Lys Ala
225 230 235 240
Leu Ala Ala Asp Asp Arg Val Glu Ile Cys Gln Leu Pro Val Gly Asp
245 250 255
Gly Ile Thr Leu Cys Arg Arg Ala Lys
260 265

<210> 100
<211> 363
<212> PRT
<213> Lolium perenne

<400> 100
Met Thr Val Val Glu Val Leu Ala Ala Gly Asp Ala Ala Ala Ala Ala
1 5 10 15

```
Val Ala Arg Pro Ala Gly Asn Gly Gln Thr Val Cys Val Thr Gly Ala
            20                  25                  30
Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu Leu Glu Lys Gly
        35                  40                  45
Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp Pro Lys Asn Ala
    50                  55                  60
His Leu Arg Ala Leu Asp Gly Ala Ala Asp Arg Leu Val Leu Cys Lys
65                  70                  75                  80
Ala Asp Leu Leu Asp Tyr Asp Ala Ile Arg Arg Ala Ile Asp Gly Cys
                85                  90                  95
His Gly Val Phe His Thr Ala Ser Pro Val Thr Asp Asp Pro Glu Gln
            100                 105                 110
Met Val Glu Pro Ala Val Arg Gly Thr Gln Tyr Val Ile Asp Ala Ala
        115                 120                 125
Ala Glu Ala Gly Thr Val Arg Arg Met Val Leu Thr Ser Ser Ile Gly
    130                 135                 140
Ala Val Thr Met His Pro Asn Arg Gly Pro Asp Val Val Val Asp Glu
145                 150                 155                 160
Ser Cys Trp Ser Asp Leu Asp Phe Cys Lys Lys Thr Arg Asn Trp Tyr
                165                 170                 175
Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala Ser Glu Leu Ala Arg
            180                 185                 190
Gln Arg Gly Val Asp Leu Val Val Val Asn Pro Val Leu Val Ile Gly
        195                 200                 205
Pro Leu Leu Gln Pro Thr Val Asn Ala Ser Ile Gly His Ile Leu Lys
    210                 215                 220
Tyr Leu Asp Gly Ser Ala Ser Lys Phe Ala Asn Ala Val Gln Ala Tyr
225                 230                 235                 240
Val Asp Val Arg Asp Val Ala Asp Ala His Leu Arg Val Phe Glu Cys
                245                 250                 255
Ala Ala Ala Ser Gly Arg His Leu Cys Ala Glu Arg Val Leu His Arg
            260                 265                 270
Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe Pro Glu Tyr Pro Val
        275                 280                 285
Pro Thr Arg Cys Ser Asp Glu Ala Asn Pro Arg Lys Gln Pro Tyr Lys
    290                 295                 300
Met Ser Asn Gln Lys Leu Gln Asp Leu Gly Leu Glu Phe Arg Pro Val
305                 310                 315                 320
Ser Gln Ser Leu Tyr Glu Thr Val Lys Ser Leu Gln Glu Lys Gly His
                325                 330                 335
Leu Pro Val Leu Ser Glu Gln Ala Glu Ala Asp Lys Glu Thr Leu Ala
            340                 345                 350
Ala Glu Leu Gln Ala Gly Val Thr Ile Arg Ala
        355                 360

<210> 101
<211> 342
<212> PRT
<213> Festuca arundinacea

<400> 101
Met Thr Val Val Asp Ala Ala Ala Pro Gln Leu Pro Gly His Gly Gln
 1               5                  10                  15
Thr Val Cys Val Thr Gly Ala Ala Gly Tyr Ile Ala Ser Gly Leu Val
            20                  25                  30
Lys Leu Leu Leu Glu Arg Gly Tyr Thr Val Lys Gly Thr Val Arg Asn
        35                  40                  45
Pro Asp Asp Pro Lys Asn Ala His Leu Lys Ala Leu Asp Gly Ala Thr
    50                  55                  60
Glu Arg Leu Ile Leu Cys Lys Ala Asp Leu Leu Asp Tyr Asp Ala Ile
65                  70                  75                  80
Cys Ala Ala Val Glu Gly Cys His Gly Val Phe His Thr Ala Ser Pro
                85                  90                  95
Val Thr Asp Asp Pro Glu Gln Met Val Glu Pro Ala Val Arg Gly Thr
            100                 105                 110
```

Glu Tyr Val Ile Asn Ala Ala Ala Asp Ala Gly Thr Val Arg Arg Val
115 120 125
Val Phe Thr Ser Ser Ile Gly Ala Ile Thr Met Asp Pro Asn Arg Gly
130 135 140
Pro Asp Val Val Val Asn Glu Ser Cys Trp Ser Asp Leu Glu Phe Cys
145 150 155 160
Lys Lys Thr Lys Asn Trp Tyr Cys Tyr Gly Lys Ala Val Ala Glu Gln
165 170 175
Ala Ala Trp Glu Ala Ala Arg Lys Arg Gly Ile Asp Leu Val Val Val
180 185 190
Asn Pro Val Leu Val Val Gly Pro Leu Leu Gln Pro Thr Val Asn Ala
195 200 205
Ser Ala Ala His Ile Leu Lys Tyr Leu Asp Gly Ser Ala Lys Lys Tyr
210 215 220
Ala Asn Ala Val Gln Ser Tyr Val Asp Val Arg Asp Val Ala Gly Ala
225 230 235 240
His Ile Arg Val Phe Glu Ala Pro Glu Ala Ser Gly Arg Tyr Leu Cys
245 250 255
Ala Glu Arg Val Leu His Arg Gly Asp Val Val Gln Ile Leu Ser Lys
260 265 270
Leu Phe Pro Glu Tyr Pro Val Pro Thr Arg Cys Ser Asp Glu Val Asn
275 280 285
Pro Arg Lys Gln Pro Tyr Lys Met Ser Asn Gln Lys Leu Gln Asp Leu
290 295 300
Gly Leu Gln Phe Thr Pro Val Asn Asp Ser Leu Tyr Glu Thr Val Lys
305 310 315 320
Ser Leu Gln Glu Lys Gly His Leu Leu Val Pro Ser Lys Pro Glu Gly
325 330 335
Leu Asn Gly Val Thr Ala
340

<210> 102
<211> 360
<212> PRT
<213> Festuca arundinacea

<400> 102
Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Gln Glu Ala
1 5 10 15
Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
20 25 30
Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
35 40 45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
50 55 60
Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
65 70 75 80
Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
85 90 95
Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
100 105 110
Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
115 120 125
Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
130 135 140
Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
145 150 155 160
Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
165 170 175
Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
180 185 190
His Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
195 200 205
Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Ala Ile Lys Gly
210 215 220

Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
225 230 235 240
Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
245 250 255
Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
260 265 270
Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
275 280 285
Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
290 295 300
Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
305 310 315 320
Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Glu Ala Leu Ala
325 330 335
Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
340 345 350
Ala Trp Ala Ile Glu Phe Thr Lys
355 360

<210> 103
<211> 360
<212> PRT
<213> FLolium perenne

<400> 103
Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Glu Asp Ala
1 5 10 15
Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Val Leu Pro Met Thr
20 25 30
Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
35 40 45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
50 55 60
Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Ile Leu Arg Leu
65 70 75 80
Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
85 90 95
Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
100 105 110
Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
115 120 125
Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
130 135 140
Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
145 150 155 160
Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
165 170 175
Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
180 185 190
His Gly Phe Glu Gly Leu Gly Ser Leu Val Asp Val Gly Gly Gly Val
195 200 205
Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Thr Ile Lys Gly
210 215 220
Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
225 230 235 240
Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
245 250 255
Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
260 265 270
Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
275 280 285
Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Asn
290 295 300
Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
305 310 315 320

```
Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Gln Ala Leu Ala
                325                 330                 335
Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
            340                 345                 350
Ala Trp Ala Ile Glu Phe Thr Lys
        355                 360
```

<210> 104
<211> 360
<212> PRT
<213> Festuca arundinacea

<400> 104

```
Met Gly Ser Thr Ala Ala Asp Met Thr Ala Ser Ala Asp Glu Glu Ala
1               5                   10                  15
Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
            20                  25                  30
Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
        35                  40                  45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
    50                  55                  60
Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
65                  70                  75                  80
Leu Ala Ser Tyr Asn Val Val Ser Cys Leu Val Glu Glu Gly Lys Asp
                85                  90                  95
Gly Arg Leu Ser Arg Asn Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
            100                 105                 110
Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
        115                 120                 125
Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
    130                 135                 140
Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
145                 150                 155                 160
Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
                165                 170                 175
Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
            180                 185                 190
Asp Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
        195                 200                 205
Gly Ala Thr Val Ala Ala Ile Thr Ala His Tyr Pro Ala Ile Lys Gly
    210                 215                 220
Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Pro Phe Pro
225                 230                 235                 240
Gly Val Thr His Val Gly Gly Asp Met Phe Lys Lys Val Pro Ser Gly
                245                 250                 255
Asp Ala Ile Met Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
            260                 265                 270
Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
        275                 280                 285
Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
    290                 295                 300
Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
305                 310                 315                 320
Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Glu Ala Leu Ala
                325                 330                 335
Arg Gly Ala Gly Phe Ala Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
            340                 345                 350
Ala Trp Ala Ile Glu Phe Thr Lys
        355                 360
```

<210> 105
<211> 361
<212> PRT
<213> Lolium perenne

<400> 105
Met Gly Ser Thr Ala Ala Glu Ile Ala Ala Ser Ala Asp Glu Glu Ala
1   5   10   15
Cys Leu Tyr Ala Leu Gln Leu Gly Ser Ser Ser Ile Leu Pro Met Thr
            20   25   30
Leu Lys Asn Thr Ile Glu Leu Gly Leu Leu Glu Thr Leu Met Ala Ala
        35   40   45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Cys
    50   55   60
Ala Ala Lys Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg
65   70   75   80
Leu Leu Ala Ser Tyr Asn Leu Val Ser Cys Leu Val Glu Glu Gly Thr
                85   90   95
Asp Gly Arg Leu Ser Arg Arg Tyr Gly Ala Ala Pro Val Cys Lys Phe
            100   105   110
Leu Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met
        115   120   125
Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala
    130   135   140
Val Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala
145   150   155   160
Phe Glu Tyr His Gly Thr Asp Leu Arg Phe Asn Arg Val Phe Asn Glu
                165   170   175
Ala Met Lys Asn Asn Ser Ile Ile Ile Thr Lys Lys Leu Leu Gln Leu
            180   185   190
Tyr Asp Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly
        195   200   205
Val Gly Ala Thr Val Ala Ala Ile Thr Ala His Tyr Pro Thr Ile Lys
    210   215   220
Gly Ile Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Pro Phe
225   230   235   240
Pro Gly Val Thr His Ile Gly Gly Asp Met Phe Lys Lys Val Pro Ser
                245   250   255
Gly Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln
            260   265   270
His Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Val His
        275   280   285
Gly Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala
    290   295   300
Lys Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala
305   310   315   320
His Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Tyr Glu Ala Leu
                325   330   335
Ala Arg Gly Ala Gly Phe Ala Gly Phe Lys Ser Thr Tyr Ile Tyr Ala
            340   345   350
Asn Ala Trp Ala Ile Glu Phe Thr Lys
        355   360

<210> 106
<211> 532
<212> PRT
<213> Lolium perenne

<400> 106
Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Ile Gln Asp Pro Leu
1   5   10   15
Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
            20   25   30
Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
        35   40   45
Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
    50   55   60
Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
65   70   75   80
Lys Leu His Thr Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
                85   90   95

```
Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
            100                 105                 110
Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
        115                 120                 125
Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
    130                 135                 140
Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
145                 150                 155                 160
Ala Leu Val Arg Ala Val Ala Arg Arg Thr Gly Glu Ser Val Asp Leu
                165                 170                 175
Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
            180                 185                 190
Phe Gly Ala Gly Ala Val Ala Ala Asp Ala Glu Glu Gly Asp Gly Ala
        195                 200                 205
Gly Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu
    210                 215                 220
Phe Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala
225                 230                 235                 240
Asp Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Asn Ala Leu
                245                 250                 255
Asp Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys
            260                 265                 270
Asn Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe
        275                 280                 285
Leu Pro Glu Ala Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp
    290                 295                 300
Asp Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile
305                 310                 315                 320
Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile
                325                 330                 335
Glu Trp Ala Met Ala Glu Met Met His Ser Pro Asp Asp Leu Arg Arg
            340                 345                 350
Leu Gln Gln Glu Leu Val Asp Val Val Gly Leu Asp Arg Asn Val Asp
        355                 360                 365
Glu Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu
    370                 375                 380
Thr Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala
385                 390                 395                 400
Glu Asp Cys Val Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val
                405                 410                 415
Met Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Arg Ala Trp Lys Asp
            420                 425                 430
Ala Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala
        435                 440                 445
Ala Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly
    450                 455                 460
Ser Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu
465                 470                 475                 480
Glu Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro
                485                 490                 495
Asp Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu
            500                 505                 510
Thr Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu
        515                 520                 525
Ala Cys Thr Gln
    530
```

<210> 107
<211> 542
<212> PRT
<213> Festuca arundinacea

<400> 107

```
Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Leu Gln Glu Pro Leu
1               5                   10                  15
```

Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
20 25 30
Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
35 40 45
Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
50 55 60
Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
65 70 75 80
Lys Leu His Ala Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
85 90 95
Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
100 105 110
Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
115 120 125
Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
130 135 140
Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
145 150 155 160
Ala Leu Val Arg Ala Val Ala Arg Arg Ser Gly Glu Ser Val Asp Leu
165 170 175
Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
180 185 190
Phe Gly Ala Gly Ala Val Ala Gly Asp Gly Asp Gly Asp Gly Ala Gly
195 200 205
Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu Phe
210 215 220
Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala Asp
225 230 235 240
Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Ala Ala Leu Asp
245 250 255
Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys Asn
260 265 270
Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe Leu
275 280 285
Pro Glu Thr Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp Asp
290 295 300
Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile Ile
305 310 315 320
Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile Glu
325 330 335
Trp Ala Met Ala Glu Met Met His Ser Pro Gly Asp Leu Arg Arg Leu
340 345 350
Gln Gln Glu Leu Ala Asp Val Val Gly Leu Asp Arg Asn Val Asp Glu
355 360 365
Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu Thr
370 375 380
Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala Glu
385 390 395 400
Asp Cys Ile Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val Met
405 410 415
Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Lys Ala Trp Lys Asp Ala
420 425 430
Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala Ala
435 440 445
Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly Ser
450 455 460
Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu Glu
465 470 475 480
Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro Asp
485 490 495
Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu Thr
500 505 510
Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu Ala
515 520 525
Cys Thr Gln Leu Leu Gly Ala Asp Asp Ala Gly Arg Gln Ala
530 535 540

<210> 108
<211> 711
<212> PRT
<213> Lolium perenne

<400> 108
Met Glu Ser Glu Asn Val Ala Ala Asn Gly Asp Gly Leu Cys Val Ala
1 5 10 15
Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala Glu Glu
20 25 30
Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu Glu Tyr
35 40 45
Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile Ala Met
50 55 60
Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu Asp Glu
65 70 75 80
Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met Asn Ser
85 90 95
Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala
100 105 110
Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg Glu Leu
115 120 125
Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp Gly His
130 135 140
Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg Val Asn
145 150 155 160
Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Thr
165 170 175
Val Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro Leu Arg
180 185 190
Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
195 200 205
Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro Asp Gly
210 215 220
Thr Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile Gln His
225 230 235 240
Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val Asn Gly
245 250 255
Thr Ala Val Gly Ser Gly Leu Ala Ser Met Val Leu Phe Glu Ala Asn
260 265 270
Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys Glu Val
275 280 285
Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys Leu Lys
290 295 300
His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His Ile Leu
305 310 315 320
Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu Leu Asp
325 330 335
Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro
340 345 350
Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr Lys Ser
355 360 365
Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val
370 375 380
Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr Pro Ile
385 390 395 400
Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys
405 410 415
Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn
420 425 430
Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Tyr
435 440 445
Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu
450 455 460

```
Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln
465                 470                 475                 480
His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr
            485                 490                 495
Ser Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe Leu Val
            500                 505                 510
Ala Leu Cys Gln Ala Ile Asp Leu Arg His Leu Glu Glu Asn Val Lys
        515                 520                 525
Asn Ala Val Lys Asn Cys Val Lys Met Val Ala Arg Lys Thr Leu Ser
    530                 535                 540
Thr Asn Asp Ser Gly His Leu His Ser Ala Arg Phe Cys Glu Lys Asp
545                 550                 555                 560
Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala Asp Asp
            565                 570                 575
Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala Val Leu
            580                 585                 590
Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Arg Asp Val Gln Thr
        595                 600                 605
Ser Val Phe Ala Lys Leu Ala Ala Phe Glu Gln Glu Leu Arg Ala Val
    610                 615                 620
Leu Pro Arg Glu Val Glu Ser Ala Arg Cys Ala Val Glu Asn Gly Thr
625                 630                 635                 640
Ala Ala Gln Gln Asn Arg Ile Thr Glu Cys Arg Ser Tyr Pro Leu Tyr
            645                 650                 655
Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly Glu Lys
            660                 665                 670
Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala Met Asn
        675                 680                 685
Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu Trp Asn
    690                 695                 700
Gly Glu Pro Leu Pro Ile Cys
705                 710
```

<210> 109
<211> 713
<212> PRT
<213> Festuca arundinacea

<400> 109

```
Met Glu Cys Glu Asn Gly His Val Ala Ala Asn Gly Asp Gly Leu Cys
 1               5                  10                  15
Val Ala Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala
            20                  25                  30
Glu Glu Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu
        35                  40                  45
Glu Tyr Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile
    50                  55                  60
Ala Met Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu
65                  70                  75                  80
Asp Glu Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met
                85                  90                  95
Asn Ser Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe
            100                 105                 110
Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg
        115                 120                 125
Glu Leu Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp
    130                 135                 140
Gly His Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg
145                 150                 155                 160
Val Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu
                165                 170                 175
Glu Thr Ile Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro
            180                 185                 190
Tyr Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
        195                 200                 205
```

```
Ile Ala Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro
    210                 215                 220
Asp Gly Ser Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile
225                 230                 235                 240
Gln His Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val
                245                 250                 255
Asn Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu
            260                 265                 270
Ala Asn Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys
        275                 280                 285
Glu Val Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys
    290                 295                 300
Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ile Met Glu His
305                 310                 315                 320
Ile Leu Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu
                325                 330                 335
Leu Asp Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr
            340                 345                 350
Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr
        355                 360                 365
Lys Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile
    370                 375                 380
Asp Val Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr
385                 390                 395                 400
Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile
                405                 410                 415
Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr
            420                 425                 430
Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu
        435                 440                 445
Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser
    450                 455                 460
Glu Leu Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala
465                 470                 475                 480
Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg
                485                 490                 495
Lys Thr Ala Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe
            500                 505                 510
Met Val Ala Leu Cys Gln Ala Ile Asp Leu Arg His Ile Glu Glu Asn
        515                 520                 525
Val Lys Asn Ala Val Lys Asn Cys Val Lys Thr Val Ala Arg Lys Thr
    530                 535                 540
Leu Ser Thr Asn Asp Ser Gly His Leu His Asn Ala Arg Phe Cys Glu
545                 550                 555                 560
Lys Asp Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala
                565                 570                 575
Asp Asp Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala
            580                 585                 590
Val Leu Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Gln Asp Val
        595                 600                 605
Gln Thr Ser Val Phe Ala Lys Leu Ala Thr Phe Glu Gln Glu Leu Arg
    610                 615                 620
Ala Val Leu Pro Lys Glu Val Glu Ser Ala Arg Cys Ser Val Glu Asn
625                 630                 635                 640
Gly Thr Ala Ala Gln Gln Asn Arg Ile Ser Glu Cys Arg Ser Tyr Pro
                645                 650                 655
Leu Tyr Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly
            660                 665                 670
Glu Lys Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala
        675                 680                 685
Met Asn Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu
    690                 695                 700
Trp Asn Gly Glu Pro Leu Pro Ile Cys
705                 710
```

<210> 110
<211> 323
<212> PRT
<213> Festuca arundinacea

<400> 110
Met Ala Phe Ser Gly Ser Val Ser Gly Val Val Leu Val Val Ala Ile
1 5 10 15
Leu Leu Leu Gly Leu Ala Ala Ala Ala Ser Ala Gln Leu Ser Ala Thr
20 25 30
Phe Tyr Asp Ala Ser Cys Pro Ser Ala Leu Ala Thr Ile Lys Ser Ala
35 40 45
Val Thr Ala Ala Val Asn Asn Glu Ala Arg Met Gly Ala Ser Leu Leu
50 55 60
Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Ala Ser Val
65 70 75 80
Leu Leu Asn Asp Thr Ala Asn Phe Thr Gly Glu Gln Thr Ala Phe Pro
85 90 95
Asn Arg Asn Ser Ile Arg Gly Leu Asn Val Ile Asp Asn Val Lys Ala
100 105 110
Gln Val Glu Ala Val Cys Thr Gln Thr Val Ser Cys Ala Asp Ile Leu
115 120 125
Ala Val Ala Ala Arg Asp Ser Ile Val Ala Leu Gly Gly Pro Ser Tyr
130 135 140
Thr Val Pro Leu Gly Arg Arg Asp Ser Thr Thr Ala Ser Leu Ser Glu
145 150 155 160
Ala Asn Arg Asp Leu Pro Pro Pro Ser Ser Asp Leu Ala Asp Leu Val
165 170 175
Gly Asn Phe Ser Arg Lys Gly Leu Ser Val Thr Asp Met Val Ala Leu
180 185 190
Ser Gly Ala His Thr Ile Gly Arg Ala Ala Cys Leu Asn Phe Arg Ser
195 200 205
Arg Ile Tyr Gly Glu Ser Asn Ile Ala Pro Ala Tyr Ala Ala Ser Leu
210 215 220
Gln Ala Asn Cys Pro Gln Ser Ala Pro Asn Gly Asp Gly Thr Leu Ala
225 230 235 240
Pro Leu Asp Val Ser Thr Pro Asp Ala Phe Asp Asn Ala Tyr Tyr Gly
245 250 255
Asn Leu Leu Ser Gln Gln Gly Leu Leu His Ser Asp Gln Gln Leu Phe
260 265 270
Asn Gly Gly Ser Thr Asp Ser Leu Val Ser Thr Tyr Ala Ser Asn Ala
275 280 285
Ala Gln Phe Ser Gly Asp Phe Ala Ala Ala Met Val Asn Met Gly Asn
290 295 300
Ile Gly Val Leu Thr Gly Ala Gln Gly Glu Ile Arg Leu Asn Cys Gly
305 310 315 320
Lys Val Asn

<210> 111
<211> 344
<212> PRT
<213> Lolium perenne

<400> 111
Met Ala Ser Ser Ser Ser Pro Phe Ser Arg Val Ser Gln Leu Ala Val
1 5 10 15
Lys Ala Thr Val Leu Ala Ala Val Cys Leu Leu Leu His Gly Gly Gly
20 25 30
Gly Ser Ser Ala Ser Ala Ala Glu Leu Cys Val Ser Tyr Tyr Asp His
35 40 45
Thr Cys Pro Asp Ala Tyr Lys Ile Val Gln Gly Val Leu Val Glu Ala
50 55 60
His Lys Ser Asp Pro Arg Ile Phe Ala Ser Leu Ile Arg Leu His Phe
65 70 75 80

```
His Asp Cys Phe Val Leu Gly Cys Asp Gly Ser Leu Leu Leu Asp Thr
                85                  90                  95
Phe Pro Gly Phe Gln Ser Glu Lys Asp Ala Arg Pro Asn Asn Asn Ser
            100                 105                 110
Ala Arg Gly Tyr Pro Val Val Asp Ala Ala Lys Ala Ala Leu Glu Lys
        115                 120                 125
Ala Cys Pro Gly Val Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala
    130                 135                 140
Glu Ile Ser Val Gln Leu Ser Gly Gly Pro Gly Trp Gly Val Leu Leu
145                 150                 155                 160
Gly Arg Leu Asp Gly Lys Thr Ser Ser Ile Ala Gly Ala Gln Asn Leu
                165                 170                 175
Pro Gly Pro Phe Asp Gly Leu Lys Asn Leu Thr Leu Lys Phe Gln Ala
            180                 185                 190
Val Asn Leu Asp Val Thr Asp Leu Val Ala Leu Ser Gly Ala His Thr
        195                 200                 205
Phe Gly Arg Val Lys Cys Arg Phe Val Thr Asn Arg Leu Tyr Asn Phe
    210                 215                 220
Ser Gly Thr Asn Gln Pro Asp Pro Thr Leu Asn Ala Ala Tyr Arg Ala
225                 230                 235                 240
Phe Leu Ser Thr Arg Cys Pro Arg Asn Gly Asp Ala Asn Ser Leu Asn
                245                 250                 255
Asp Leu Asp Pro Thr Thr Pro Asp Thr Phe Asp Lys Asn Tyr Phe Thr
            260                 265                 270
Asn Leu Glu Lys Asn Arg Gly Phe Leu Asp Ser Asp Gln Gln Leu Lys
        275                 280                 285
Ser Asp Pro Gly Ala Leu Thr Thr Thr Ala Pro Ile Val Asp Arg Phe
    290                 295                 300
Ala Ser Ser Gln Asp Ala Phe Phe Lys Ser Phe Ala Trp Ser Met Ile
305                 310                 315                 320
Lys Met Gly Asn Ile Leu Pro Ile Thr Asp Pro Ser Arg Gly Glu Val
                325                 330                 335
Arg Lys His Cys Ala Phe Val Asn
            340

&lt;210&gt; 112
&lt;211&gt; 326
&lt;212&gt; PRT
&lt;213&gt; Festuca arundinacea

&lt;400&gt; 112
Met Ala Thr Arg Gly Val Met Val Ala Leu Leu Leu Ala Ala Val Ala
1               5                   10                  15
Ala Ser Cys Ala His Ala Gln Leu His Glu Lys Phe Tyr Ser Glu Ser
            20                  25                  30
Cys Pro Ser Val Glu Asp Val Val Arg Lys Glu Met Val Met Ala Leu
        35                  40                  45
Ser Leu Ala Pro Ser Leu Ala Ala Pro Leu Leu Arg Met His Phe His
    50                  55                  60
Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp Ser Ala
65                  70                  75                  80
Asn Lys Thr Ala Glu Lys Asp Ala Leu Pro Asn Gln Thr Leu Arg Gly
                85                  90                  95
Phe Asp Phe Val Glu Arg Val Lys Ala Ala Val Glu Lys Ala Cys Pro
            100                 105                 110
Asp Thr Val Ser Cys Ala Asp Val Val Thr Leu Ile Ala Arg Asp Ala
        115                 120                 125
Val Trp Leu Ser Lys Gly Pro Phe Trp Glu Val Pro Leu Gly Arg Arg
    130                 135                 140
Asp Gly Ser Val Ser Ile Ser Asn Glu Thr Asp Ala Leu Pro Pro Pro
145                 150                 155                 160
Thr Ala Asn Ile Thr Val Leu Thr Gln Leu Phe Ala Ala Lys Asn Leu
                165                 170                 175
Asp Ile Lys Asp Leu Val Val Leu Ser Ala Ala His Thr Ile Gly Thr
            180                 185                 190
```

```
Ser His Cys Phe Ser Phe Ser Asp Arg Leu Tyr Asn Phe Thr Gly Leu
        195                 200                 205
Asp Asn Ala Ser Asp Ile Asp Pro Thr Leu Glu Pro Phe Tyr Met Ala
    210                 215                 220
Lys Leu Lys Ser Lys Cys Thr Ser Leu Asp Asp Asn Ser Thr Leu Val
225                 230                 235                 240
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Asp Tyr Phe Lys
                245                 250                 255
Leu Val Ser Lys Arg Arg Gly Leu Phe His Ser Asp Gly Ala Leu Leu
            260                 265                 270
Thr Asp Ala Phe Thr Arg Ala Tyr Ile Leu Arg His Ala Thr Gly Ala
        275                 280                 285
Phe Lys Asp Glu Phe Phe Ala Asp Phe Ala Val Ser Met Val Lys Met
    290                 295                 300
Gly Asn Thr Asp Val Leu Thr Gly Ser Gln Gly Glu Ile Arg Lys Lys
305                 310                 315                 320
Cys Ser Val Val Asn His
                325
```

<210> 113
<211> 358
<212> PRT
<213> Lolium perenne

<400> 113

```
Met Ala Ser Ser Arg Val Leu Leu Leu Val Val Ala Ala Leu Ala Ile
 1               5                  10                  15
Ser Val Ser Ala Thr Ala Ala Ala Thr Lys Ile Ser Ala Pro Leu Pro
            20                  25                  30
Pro Leu Ala Lys Gly Leu Asn Phe Asp Phe Tyr Lys Ala Thr Cys Pro
        35                  40                  45
Gln Ala Glu Ser Ile Val Phe Asn Phe Leu Arg Asp Ala Ile Arg Lys
    50                  55                  60
Asp Val Gly Leu Ala Ala Ala Leu Leu Arg Ile His Phe His Asp Cys
65                  70                  75                  80
Phe Val Gln Gly Cys Asp Gly Ser Val Leu Leu Asp Lys Thr Gly Gly
                85                  90                  95
Thr Asp Ser Glu Lys Ile Ala Pro Pro Asn Val Thr Leu Arg Pro Thr
            100                 105                 110
Ala Phe Lys Ala Ile Asn Asp Leu Arg Ala Leu Leu Ala Lys Ala Cys
        115                 120                 125
Gly Ala Val Val Ser Cys Ala Asp Ile Ala Ala Leu Ala Ala Arg Asp
    130                 135                 140
Ser Val His Leu Ala Gly Gly Pro His Tyr Pro Val Pro Leu Gly Arg
145                 150                 155                 160
Arg Asp Gly Leu Ala Pro Ala Asn Leu Thr Thr Ile Leu Asn Ala Leu
                165                 170                 175
Pro Ala Pro Ser Ser Asn Val Thr Thr Leu Leu Arg Phe Leu Ala Lys
            180                 185                 190
Ile Ser Leu Asp Ala Asn Asp Leu Val Ala Leu Ser Gly Ala His Thr
        195                 200                 205
Leu Gly Ile Ala His Cys Thr Ser Phe Gln Glu Arg Leu Phe Pro Gln
    210                 215                 220
Asn Asp Val Thr Leu Asn Lys Trp Phe Ala Ser Gln Leu Arg Leu Thr
225                 230                 235                 240
Cys Pro Ala Leu Asn Thr Asp Asn Thr Thr Asn Asn Asp Ile Arg Thr
                245                 250                 255
Pro Asn Val Phe Asp Asn Lys Tyr Tyr Val Asp Leu Leu Asn Arg Gln
            260                 265                 270
Gly Leu Phe Thr Ser Asp Gln Asp Leu His Thr Asp Ala Arg Thr Lys
        275                 280                 285
Pro Thr Val Thr Arg Phe Ala Val Asp Gln Ala Ala Phe Phe Asp Gln
    290                 295                 300
Phe Val Phe Ser Val Val Lys Met Gly Gln Ile Asn Val Leu Thr Gly
305                 310                 315                 320
```

```
Ser Gln Gly Gln Ile Arg Asn Asp Cys Ser Ala Pro Asn Lys Gly Arg
                325                 330                 335
Thr Asn Asp Asp Leu Pro Trp Ser Val Leu Glu Thr Val Thr Glu Ala
            340                 345                 350
Ala Gln Ser Leu Val Leu
        355
```

<210> 114
<211> 344
<212> PRT
<213> Lolium perenne

<400> 114

```
Met Thr Thr Met Gly Gly Ser Ser Ile Leu Pro Ala Pro Thr Val Ala
1               5                   10                  15
Thr Thr Ala Leu Val Leu Leu Ile Val Leu Phe Ala Ser Pro Ala Thr
            20                  25                  30
Val Ala Lys Gly Ser Gly Leu Ser Val Gly Phe Tyr Lys Lys Leu Cys
        35                  40                  45
Pro Lys Ala Glu Lys Val Val Arg Arg Thr Val Thr Lys Ala Phe Glu
    50                  55                  60
Lys Glu Pro Gly Thr Pro Ala Asp Ile Ile Arg Leu Phe Phe His Asp
65                  70                  75                  80
Cys Phe Val Arg Gly Cys Asp Ala Ser Val Leu Leu Glu Ser Thr Pro
                85                  90                  95
Gly Arg Met Ala Glu Arg Asp Ser Lys Ala Asn Asn Pro Ser Leu Asp
            100                 105                 110
Gly Phe Glu Val Ile Ser Asp Ala Lys Glu Thr Leu Glu Lys Leu Cys
        115                 120                 125
Pro Gln Thr Val Ser Cys Ala Asp Ile Leu Ala Leu Ala Ala Arg Asp
    130                 135                 140
Gly Ala Tyr Leu Ala Ser Gly Leu Asp Tyr Ala Val Pro Thr Gly Arg
145                 150                 155                 160
Arg Asp Gly Leu Val Ser Lys Glu Asp Glu Val Leu Pro Ser Val Pro
                165                 170                 175
His Pro Asp Phe Asn His Ser Gln Leu Val Glu Asn Phe Thr Ala Lys
            180                 185                 190
Gly Phe Thr Ala Glu Glu Met Val Thr Leu Ser Gly Ala His Thr Ile
        195                 200                 205
Gly Thr Ser His Cys Ser Ser Phe Thr Asp Arg Leu Tyr Asn Phe Ser
    210                 215                 220
Gln Gly Gly Ala Leu Thr Thr Asp Pro Ala Leu Pro Ala Ala Tyr Ala
225                 230                 235                 240
Ala Leu Leu Lys Glu Lys Cys Pro Pro Glu Thr Ala Ala Gln Asn Asp
                245                 250                 255
Thr Thr Met Val Gln Leu Asp Asp Val Thr Pro Phe Val Met Asp Asn
            260                 265                 270
Gln Tyr Tyr Lys Asn Leu Leu Ala Gly Thr Val Pro Leu Gly Ser Asp
        275                 280                 285
Val Ala Leu Met Glu Ser Pro Asp Thr Ala Ala Leu Val Glu Leu Tyr
    290                 295                 300
Ala Arg Glu Pro Ala Glu Tyr Trp Ala Lys Arg Phe Val Ala Ala Met
305                 310                 315                 320
Val Lys Val Ser Glu Met Glu Val Leu Thr Gly Ala Glu Gly Glu Ile
                325                 330                 335
Arg Leu Asn Cys Ser Lys Val Asn
            340
```

<210> 115
<211> 293
<212> PRT
<213> Lolium perenne

<400> 115

```
Thr Arg Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu Thr
1               5                   10                  15
```

Ile Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met Gly
20 25 30
Ala Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys
35 40 45
Asp Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu Lys
50 55 60
Gly Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile Asp
65 70 75 80
Lys Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser Cys
85 90 95
Ala Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu Gly
100 105 110
Gly Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr Ala
115 120 125
Ser Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn Leu
130 135 140
Asn Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr Asp
145 150 155 160
Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln
165 170 175
Asn Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala Phe
180 185 190
Ala Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly Asn
195 200 205
Leu Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly Tyr
210 215 220
Phe Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln Ala
225 230 235 240
Leu Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala Ser
245 250 255
Asn Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Ala Met Val Lys Leu
260 265 270
Ser Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val Asn
275 280 285
Cys Arg Ala Val Asn
290

<210> 116
<211> 311
<212> PRT
<213> Festuca arundinacea

<400> 116
Met Ala Ser Ala Ser Cys Ile Ser Leu Val Leu Leu Val Ala Leu Ala
1 5 10 15
Ala Thr Ala Ala Ser Ala Gln Leu Ser Ser Thr Phe Tyr Asp Thr Ser
20 25 30
Cys Pro Arg Ala Leu Ala Thr Ile Lys Ser Gly Val Ala Ala Ala Val
35 40 45
Ser Ser Asn Pro Arg Met Gly Ala Ser Leu Leu Arg Leu His Phe His
50 55 60
Asp Cys Phe Val Asn Gly Cys Asp Ala Ser Val Leu Leu Ser Gly Asn
65 70 75 80
Glu Gln Asn Ala Pro Ala Asn Ala Gly Ser Leu Phe Gly Phe Gly Val
85 90 95
Ile Asp Asn Ile Lys Thr Gln Leu Glu Gly Ile Cys Lys Gln Thr Val
100 105 110
Ser Cys Ala Asp Ile Leu Thr Val Ala Ala Arg Asp Ser Val Val Ala
115 120 125
Leu Gly Gly Pro Ser Trp Thr Val Pro Leu Gly Arg Arg Asp Ser Thr
130 135 140
Ser Ala Thr Gly Asn Thr Gly Asp Leu Pro Gly Pro Gly Ser Ser Leu
145 150 155 160
Ala Gln Leu Gln Ala Ala Phe Ala Lys Lys Asn Leu Asn Thr Val Asp
165 170 175

Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln
180 185 190
Asn Phe Arg Ser Arg Ile Tyr Gly Gly Asp Ser Asn Ile Asn Ala Ala
195 200 205
Phe Ala Thr Ser Leu Lys Ala Asn Cys Pro Gln Ser Gly Gly Asn Gly
210 215 220
Asn Leu Ala Ala Leu Asp Ala Thr Thr Ala Asn Ala Phe Asp Asn Ala
225 230 235 240
Tyr Tyr Thr Asn Leu Leu Ser Gln Lys Gly Leu Leu His Ser Asp Gln
245 250 255
Val Leu Phe Asn Asn Gly Ser Thr Asp Asn Thr Val Arg Asn Phe Ala
260 265 270
Ser Ser Gly Ala Ala Phe Ser Ser Ala Phe Ala Thr Ala Met Ile Lys
275 280 285
Met Gly Asn Ile Ser Pro Leu Thr Gly Thr Gln Gly Gln Ile Arg Leu
290 295 300
Ser Cys Ser Lys Val Asn Ser
305 310

<210> 117
<211> 230
<212> PRT
<213> Lolium perenne

<400> 117
Met Ala Val Ser Glu Leu Glu Val Asp Gly Val Val Phe Pro Pro Leu
1 5 10 15
Ala Arg Pro Pro Gly Thr Ala His Ala His Phe Leu Ala Gly Ala Gly
20 25 30
Val Arg Gly Met Glu Leu Gly Gly Asn Phe Ile Lys Phe Thr Ala Ile
35 40 45
Gly Val Tyr Leu Gln Ala Asp Ala Ala Val Ser Ala Leu Ala Thr Lys
50 55 60
Trp Ala Gly Lys Pro Ala Asp Glu Leu Ala Ala Asp Asn Ala Phe Phe
65 70 75 80
Arg Asp Val Val Thr Gly Glu Phe Glu Lys Phe Thr Pro Val Thr Met
85 90 95
Ile Leu Pro Leu Thr Gly Ala Gln Tyr Ser Glu Lys Val Thr Glu Asn
100 105 110
Cys Val Ala Tyr Trp Lys Ala Val Gly Lys Tyr Thr Asn Ala Glu Ala
115 120 125
Ala Ala Val Asp Lys Phe Lys Glu Ala Phe Arg Thr Glu Ser Phe Pro
130 135 140
Pro Gly Ala Ser Ile Leu Phe Thr His Ser Pro Ala Gly Val Leu Thr
145 150 155 160
Val Ala Phe Ser Lys Asp Ser Ser Val Pro Glu Ser Gly Gly Val Ala
165 170 175
Ile Glu Asn Arg Pro Leu Cys Glu Ala Val Leu Glu Ser Ile Ile Gly
180 185 190
Glu His Gly Val Ser Pro Ala Ala Lys Leu Ser Leu Ala Thr Arg Val
195 200 205
Ala Glu Leu Leu Asn Glu Ala Ala Pro Val Gly Gln Ala Ala Ala Glu
210 215 220
Pro Val Ser Val Ser Ala
225 230

<210> 118
<211> 231
<212> PRT
<213> Festuca arundinacea

<400> 118
Met Ala Val Ser Glu Leu Glu Val Asp Gly Val Val Phe Pro Pro Leu
1 5 10 15
Ala Arg Pro Pro Gly Thr Ala His Ala His Phe Leu Ala Gly Ala Gly
20 25 30

```
Val Arg Gly Met Glu Leu Gly Gly Asn Phe Ile Lys Phe Thr Ala Ile
        35                  40                  45
Gly Val Tyr Leu Gln Ala Asp Ala Ala Val Ser Ala Leu Ala Ala Lys
    50                  55                  60
Trp Ala Gly Lys Pro Ala Asp Glu Leu Ala Ala Asp Asn Ala Phe Phe
65                  70                  75                  80
Arg Asp Val Val Thr Gly Glu Phe Glu Lys Phe Arg Arg Val Thr Met
                85                  90                  95
Ile Leu Pro Leu Thr Gly Ala Gln Tyr Ser Glu Lys Val Thr Glu Asn
            100                 105                 110
Cys Val Ala Tyr Trp Lys Ala Val Gly Lys Tyr Thr Asp Ala Glu Ala
        115                 120                 125
Ala Ala Val Asp Lys Phe Lys Glu Ala Phe Lys Ala Glu Ser Phe Pro
    130                 135                 140
Pro Gly Ala Ser Ile Leu Phe Thr His Ser Pro Ala Gly Val Leu Thr
145                 150                 155                 160
Val Ala Phe Ser Lys Asp Ser Ser Leu Pro Glu Ser Gly Gly Val Ala
                165                 170                 175
Ile Glu Asn Arg Pro Leu Cys Glu Ala Val Leu Lys Ser Ile Ile Gly
            180                 185                 190
Lys His Gly Val Ser Pro Ala Ala Lys Leu Ser Leu Ala Thr Arg Val
        195                 200                 205
Ala Glu Leu Leu Lys Glu Ala Ala Pro Val Gly Glu Pro Ala Val Ala
    210                 215                 220
Glu Pro Val Ser Val Ser Ala
225                 230

<210> 119
<211> 394
<212> PRT
<213> Lolium perenne

<400> 119
Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
1               5                   10                  15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
            20                  25                  30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
        35                  40                  45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
    50                  55                  60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
65                  70                  75                  80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
                85                  90                  95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
            100                 105                 110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
        115                 120                 125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
    130                 135                 140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
145                 150                 155                 160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
                165                 170                 175
Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
            180                 185                 190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
        195                 200                 205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
    210                 215                 220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
225                 230                 235                 240
Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
                245                 250                 255
```

Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
260 265 270
Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
275 280 285
Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
290 295 300
Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
305 310 315 320
Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
325 330 335
Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
340 345 350
Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
355 360 365
Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
370 375 380
Val Val Leu His Ser Met Pro Ile Ala Ala
385 390

<210> 120
<211> 196
<212> PRT
<213> Festuca arundinacea

<400> 120
Met Tyr Phe Val Ser Lys Ser Leu Ala Glu Asn Ala Ala Met Asp Tyr
1 5 10 15
Ala Lys Glu Asn Gly Val Asp Phe Ile Ser Ile Ile Pro Thr Leu Val
20 25 30
Val Gly Pro Phe Leu Ser Ala Gly Met Pro Pro Ser Leu Val Thr Ala
35 40 45
Leu Ala Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Leu Lys Gln
50 55 60
Val Gln Leu Val His Leu Asp Asp Leu Cys Asp Ser Met Thr Tyr Leu
65 70 75 80
Phe Glu His Pro Asp Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Asp
85 90 95
Thr Thr Ile His Gly Ile Ala Arg Met Leu Lys Glu Arg Phe Pro Glu
100 105 110
Tyr Asp Ile Pro Gln Lys Phe Pro Gly Ala Asp Asp Asp Leu Gln Pro
115 120 125
Ile His Phe Phe Phe Lys Lys Leu Leu Asp His Gly Phe Arg Phe Arg
130 135 140
Tyr Thr Ala Glu Asp Met Phe Asp Ala Ala Val Trp Thr Cys Arg Glu
145 150 155 160
Lys Gly Leu Ile Pro Leu Gly Ala Glu Gly Ala Gly Gly Pro Ala Ser
165 170 175
Ala Ala Gly Lys Leu Gly Ala Val Leu Val Gly Glu Gly Gln Ala Ile
180 185 190
Gly Ala Glu Thr
195

<210> 121
<211> 329
<212> PRT
<213> Lolium perenne

<400> 121
Met Ala Thr Glu Ala Lys Gly Glu Thr Val Leu Val Thr Gly Ala Ser
1 5 10 15
Gly Phe Ile Gly Ser Trp Leu Val Arg Leu Leu Leu Ala Arg Gly Tyr
20 25 30
Ser Val His Ala Ala Val Leu Asn Pro Asp Asp Lys Ala Glu Thr Asp
35 40 45
His Leu Leu Ala Leu Ala Ala Ala Ala Gly Asp Glu Gly Arg Ile Arg
50 55 60

Phe Phe Arg Cys Asp Leu Leu Asp Gly Ala Ala Met Leu Ala Ala Val
65 70 75 80
Arg Gly Cys Ser Gly Val Phe His Leu Ala Ser Pro Cys Thr Val Asn
85 90 95
Leu Val Leu Asn Pro Gln Lys Glu Leu Val Val Pro Ala Val Glu Gly
100 105 110
Thr Leu Asn Val Leu Arg Ala Ala Lys Glu Ala Gly Gly Val Arg Arg
115 120 125
Val Val Val Thr Ser Ser Val Ser Ala Leu Val Pro Cys Pro Gly Trp
130 135 140
Pro Ala Gly Glu Val Leu Asp Glu Arg Cys Trp Thr Asp Ile Asp Tyr
145 150 155 160
Cys Asp Lys Asn Gly Val Trp Tyr Pro Ala Ser Lys Ala Leu Ala Glu
165 170 175
Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Gly Leu Asp Val Val Thr
180 185 190
Val Asn Pro Gly Thr Val Leu Gly Glu Met Ile Pro Pro Arg Leu Asn
195 200 205
Ala Ser Met Ala Met Phe Leu Arg Leu Leu Glu Gly Cys Lys Glu Glu
210 215 220
Tyr Ala Asp Phe Phe Ile Gly Pro Val His Val Glu Asp Val Ala Leu
225 230 235 240
Ala His Ile Leu Leu Tyr Glu Asn Pro Ser Ala Ser Gly Arg His Leu
245 250 255
Cys Val Glu Pro Ile Cys His Trp Ser Val Phe Ala Ala Lys Val Ala
260 265 270
Glu Leu Tyr Pro Asp Tyr Lys Val Pro Lys Phe Pro Glu Asp Thr Gln
275 280 285
Pro Gly Leu Val Arg Ala Lys Ala Val Pro Lys Lys Leu Met Ala Leu
290 295 300
Gly Leu Gln Phe Thr Pro Leu Glu Lys Ile Ile Arg Asp Ala Val Glu
305 310 315 320
Ser Leu Lys Ser Arg Gly Cys Ile Ala
325

<210> 122
<211> 328
<212> PRT
<213> Lolium perenne

<400> 122
Gly Ser Thr Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe Val
1 5 10 15
Ala Ser Trp Leu Ile Lys Lys Leu Leu Glu Ser Gly Tyr His Val Ile
20 25 30
Gly Thr Val Arg Asp Pro Gly Asn Arg Arg Lys Val Gly His Leu Trp
35 40 45
Lys Leu Pro Gly Ala Asn Glu Arg Leu Gln Leu Val Arg Ala Asp Leu
50 55 60
Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Arg Ala Cys Glu Gly Val
65 70 75 80
Phe His Ile Ala Ser Pro Val Leu Gly Lys Ser Asp Ser Asn Cys Lys
85 90 95
Glu Ala Thr Leu Gly Pro Ala Ile Asn Gly Thr Leu Asn Val Leu Arg
100 105 110
Ser Cys Lys Lys Ser Pro Phe Leu Lys Arg Val Val Leu Thr Ser Ser
115 120 125
Ser Ser Ala Val Arg Ile Arg Asp Glu Thr Gln Gln Pro Glu Leu Leu
130 135 140
Trp Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys Leu Gln
145 150 155 160
Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala Leu Asp
165 170 175
Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Thr Val Leu Pro Ser Phe
180 185 190

```
Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Thr Thr Ala Ser Asp
        195                 200                 205
Ile Leu Gly Leu Leu Gln Gly Asp Thr Asp Arg Phe Thr Leu Tyr Gly
    210                 215                 220
Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Ser His Ile Leu
225                 230                 235                 240
Val Tyr Glu Thr Pro Glu Ala Thr Gly Arg Tyr Leu Cys Ser Ser Val
                245                 250                 255
Val Leu Asp Asn Asn Glu Leu Val Gly Leu Leu Ala Lys Gln Phe Pro
            260                 265                 270
Val Phe Pro Ile Pro Arg Arg Leu Lys Asn Pro Tyr Gly Lys Gln Ala
        275                 280                 285
Tyr Gln Leu Asp Thr Ser Lys Leu Gln Gly Leu Gly Leu Lys Phe Lys
    290                 295                 300
Gly Val Gln Glu Met Phe Asn Asp Cys Val Glu Ser Leu Lys Asp Gln
305                 310                 315                 320
Gly His Leu Leu Glu Cys Pro Leu
                325
```

<210> 123
<211> 369
<212> PRT
<213> Lolium perenne

<400> 123

```
Met Ala Pro Val Val Glu Arg Ala Pro Phe Leu Pro Thr Gly Glu Ala
 1               5                  10                  15
Thr Leu Arg Pro Ser Phe Val Arg Asp Glu Asp Glu Arg Pro Lys Val
            20                  25                  30
Ala His Asp Arg Phe Ser Asp Glu Val Pro Val Ile Ser Leu His Gly
        35                  40                  45
Ile Asp Asp Ala Arg Arg Thr Glu Ile Arg Asp Arg Val Ala Ala Ala
    50                  55                  60
Cys Glu Gly Trp Gly Ile Phe Gln Val Val Asp His Gly Val Asp Ala
65                  70                  75                  80
Ala Leu Ile Ala Glu Met Ala Arg Leu Ser Arg Asp Phe Phe Ala Leu
                85                  90                  95
Pro Ala Glu Asp Lys Leu Arg Tyr Asp Met Ser Gly Gly Lys Lys Gly
            100                 105                 110
Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Thr Val Gln Asp Trp
        115                 120                 125
Arg Glu Ile Val Thr Tyr Phe Ser Tyr Pro Val Lys Ala Arg Asp Tyr
    130                 135                 140
Gly Arg Trp Pro Asp Lys Pro Ala Gly Trp Arg Ala Val Val Glu Gln
145                 150                 155                 160
Tyr Ser Glu Arg Leu Met Ala Leu Ser Cys Lys Leu Leu Gly Val Leu
                165                 170                 175
Ser Glu Ala Met Gly Leu Glu Thr Glu Ala Leu Ser Lys Ala Cys Val
            180                 185                 190
Asp Met Asp Gln Lys Val Val Val Asn Phe Tyr Pro Lys Cys Pro Gln
        195                 200                 205
Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp Pro Gly Thr Ile
    210                 215                 220
Thr Leu Leu Leu Gln Asp Leu Val Gly Gly Leu Gln Ala Thr Arg Asp
225                 230                 235                 240
Gly Gly Asn Thr Trp Ile Thr Val Gln Pro Ile Ala Gly Ala Phe Val
                245                 250                 255
Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn Gly Arg Phe Lys
            260                 265                 270
Asn Ala Asp His Gln Ala Val Val Asn Gly Glu Ser Ser Arg Leu Ser
        275                 280                 285
Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Lys Val Trp Pro Leu
    290                 295                 300
Ala Val Arg Glu Gly Glu Asp Thr Ile Leu Glu Glu Pro Ile Thr Phe
305                 310                 315                 320
```

```
Thr Glu Met Tyr Arg Arg Lys Met Ala Arg Asp Leu Glu Leu Ala Lys
                325                 330                 335
Arg Lys Lys Gln Ala Lys Ala Asp Gln Leu Lys Gln Gln Leu Gln Gln
            340                 345                 350
Glu Ala Ala Pro Ala Ala Ala Pro Thr Lys Pro Leu Asn Gln Ile Leu
        355                 360                 365
Ala


<210> 124
<211> 380
<212> PRT
<213> Festuca arundinacea

<400> 124
Met Ala Ser Val Glu Asn Ala Pro Phe Leu Pro Thr Ala Ala Thr Gly
 1               5                  10                  15
Glu Ala Thr Leu Arg Pro Ser Phe Val Arg Asp Glu Asp Glu Arg Pro
            20                  25                  30
Lys Val Ala His Asp Arg Phe Ser Asp Glu Val Pro Val Ile Ser Leu
        35                  40                  45
His Gly Ile Asp Asp Gly Gly Ala Arg Arg Ala Glu Ile Arg Asp Arg
    50                  55                  60
Val Ala Ala Ala Cys Glu Gly Trp Gly Val Phe Gln Val Val Asp His
65                  70                  75                  80
Gly Val Asp Ala Ala Leu Val Ala Glu Met Ala Arg Leu Ser Arg Glu
                85                  90                  95
Phe Phe Ala Leu Pro Ala Glu Asp Lys Leu Arg Tyr Asp Met Ser Gly
            100                 105                 110
Gly Lys Lys Gly Gly Phe Ile Val Ser Ser His Leu Gln Gly Glu Thr
        115                 120                 125
Val Gln Asp Trp Arg Glu Ile Val Thr Tyr Phe Ser Tyr Pro Val Lys
    130                 135                 140
Ala Arg Asp Tyr Gly Arg Trp Pro Glu Lys Pro Ala Gly Trp Arg Ala
145                 150                 155                 160
Val Val Glu Gln Tyr Ser Glu Arg Leu Met Ala Leu Ser Cys Lys Leu
                165                 170                 175
Leu Gly Val Leu Ser Glu Ala Met Gly Leu Glu Thr Glu Ala Leu Ser
            180                 185                 190
Lys Ala Cys Val Asp Met Asp Gln Lys Val Val Val Asn Phe Tyr Pro
        195                 200                 205
Lys Cys Pro Gln Pro Asp Leu Thr Leu Gly Leu Lys Arg His Thr Asp
    210                 215                 220
Pro Gly Thr Ile Thr Leu Leu Leu Gln Asp Leu Val Gly Gly Leu Gln
225                 230                 235                 240
Ala Thr Arg Asp Gly Gly Asn Thr Trp Ile Thr Val Gln Pro Val Pro
                245                 250                 255
Gly Ala Phe Val Val Asn Leu Gly Asp His Gly His Tyr Leu Ser Asn
            260                 265                 270
Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val Val Asn Gly Glu Ser
        275                 280                 285
Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro Ala Pro Glu Ala Lys
    290                 295                 300
Val Trp Pro Leu Ala Val Arg Glu Gly Glu Asp Thr Ile Leu Glu Glu
305                 310                 315                 320
Pro Ile Thr Phe Thr Glu Met Tyr Arg Arg Lys Met Ala Cys Asp Leu
                325                 330                 335
Glu Leu Ala Lys Arg Lys Lys Gln Ala Lys Ala Asp Gln Leu Lys Gln
            340                 345                 350
Gln Leu Gln Gln Glu Gln Gln Glu Ala Val Ala Ala Ala Ala Pro Lys
        355                 360                 365
Pro Ala Thr Thr Lys Pro Leu Asn Gln Ile Leu Ala
    370                 375                 380
```

<210> 125
<211> 2105
<212> DNA
<213> Lolium perenne

<400> 125
acttagcctt cctcggaacc atcgaccggg ccgccgccga cgcgacgcga cgcgatggag 60
tccagcgccg tcgtccccgg caccacggcg ccgctgcttc cttatgcgta cgcgccgctg 120
ccgtcgtcct ccgacgacgc ccgtgaaaac agaagtagcg gcggcgtgag gtggcgcgcg 180
tgcgccgccg ttctggcggc ctcggcgttg gcggtggtgg tcgtggtcgg gctcctcgcg 240
ggcggcaggg tggatcgggt cccggccggc gcagacgtgg cgtcggccac ggtgccggcc 300
gtgccgatgg agttcccgag gagccggggc aaggacttgg gcgtgtcgga gaagtcctcc 360
ggtgcctact ccgccgacgg cgggttcccg tggagcaacg ccatgctgca gtggcagcgc 420
accgggttcc atttccagcc ggagcagcac tacatgaacg atcccaacgg ccccgtgtac 480
tacggcggat ggtaccacct cttctaccag cacaacccca agggcgacag ctggggcaac 540
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<211> 1986
<212> DNA
<213> Festuca arundinacea

<400> 135
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<210> 136
<211> 2073
<212> DNA
<213> Lolium perenne

<400> 136
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<210> 137
<211> 1888
<212> DNA
<213> Festuca arundinacea

<400> 137

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<210> 138
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<212> DNA
<213> Lolium perenne

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<210> 139
<211> 2166
<212> DNA
<213> Lolium perenne

<400> 139
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<210> 140
<211> 2137
<212> DNA
<213> Lolium perenne

<400> 140

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<210> 141
<211> 1954
<212> DNA
<213> Lolium perenne

<400> 141

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<210> 142
<211> 2039
<212> DNA
<213> Lolium perenne

<400> 142

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<210> 143
<211> 2006
<212> DNA
<213> Lolium perenne

<400> 143
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<210> 144
<211> 1789
<212> DNA
<213> Lolium perenne

<400> 144
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<210> 145
<211> 1358
<212> DNA
<213> Lolium perenne

<400> 145
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<210> 146
<211> 1051
<212> DNA
<213> Lolium perenne

<400> 146
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gacaaataat attactccta taaaaaaaaa a                                    1051
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<210> 147
<211> 1332
<212> DNA
<213> Lolium perenne

<400> 147

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<210> 148
<211> 1236
<212> DNA
<213> Festuca arundinacea

<400> 148

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<210> 149
<211> 1428
<212> DNA
<213> Festuca arundinacea

<400> 149
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aacgaaactg catatttatg tacactgcct atttatttcc tgtccttgtg tccccgtctt 1140
gttatattac atccataatc catgttaaga tggtggcatt ggtttaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 157
<211> 1530
<212> DNA
<213> Lolium perenne

<400> 157
actcattcat ctgtcgtctc ctgcttccct caagcttaga tcgattgcag ccggccgggg 60
actgttgagc taccactgcc ggtcgctggt acgagcggac gtaaggagag atccagatgg 120
ccgcgacgat gaccgtggag gaggtgagga aggcacagcg ggcggagggg ccggcgacgg 180
tgctggccat cggcacggcg acgcccgcta actgtgtcta ccaggctgac tacccggact 240
actacttcaa gatcaccaag agcgaccacc tcgccgatct caaggagaag ttcaagagga 300
tgtgcgacaa gtctcagatc aggaagaggt acatgcacct gacggaggag atcctggagg 360
agaaccccaa catgtgcgcg tacatggcgc cgtcgctgga cgcgcgccag gacatagttg 420
tcgtcgaggt cccgaagctc gggaaggcgg cggcacagaa ggcgatcaag gagtggggcc 480
agccgcggtc caagatcacc cacctcgtct tctgcactac ctctggtgtg gacatgccag 540
gcgccgacta ccagctcacc aagatgctcg gcctgcgccc gtcggtgaag cgcctcatga 600
tgtaccagca gggctgcttc gccggcggca cggtgctccg cctcgccaag gacctggctg 660
aaaacaaccg cggcgcgcgc gtgctggtgg tctgctcgga gatcacggcc gtgaccttcc 720
gcggcccgca cgagtcacac ctcgactcgc tggtcggcca ggcgctcttc ggggacggcg 780
ctgccgcggt gataatcggc gccgaccccg acgtgtccgt cgagcgcccg ctgttccagc 840
tggtgtcggc gagccagacc atcctgccgg actcggaggg cgccatcgac ggccacctca 900
gggaggtcgg cctcaccttc cacctcctca aggacgtgcc cgggctcatc tccaagaaca 960
tcgagcgcgc cctggaggaa gccttcaagc cgctcggcat cgacgactgg aactccgtct 1020
tttgggtggc gcacccgggc gggccggcga tcctcgacat ggtggaggca aaggtaaacc 1080
tcaacaagga gcggatgcgt gccaccaggc acgtcctctc cgagtacggc aacatgtcca 1140
gcgcatgcgt cctcttcatc atggacgaga tgcgcaagcg ctctgccgag gatggtcaca 1200
ccaccaccgg cgagggaatg gattggggcg tcctctttgg cttcgggccc ggcctcaccg 1260
tcgagaccgt tgtcctccac agcatgccca ttgccgctga tgccaccgct tgatcgatgg 1320
ttccatctcc gtttatctgc cacatcgatg gatacctact actactaccg ccgccgccgc 1380
tgctatccaa agtaatttgt attgtattca tgcatacctg gtttgtattt gttggtagga 1440
ttcgttccgc tattatgtcg cttgtgtcgc gtacactgtt gtatcctagt aatagtaatc 1500
aaacggagta cggtttatgt aaaaaaaaaa 1530

<210> 158
<211> 1418
<212> DNA
<213> Festuca arundinacea

<400> 158
gaaaagacag cacagaaatc tatattctac aaggcagaaa agagcagcag ggaaatcta 60
gctaaggtct tgagaggaag atgaagcagg aggtgaagag cgagatgaac ggcgagacga 120
tgagcggcaa caaagggccg gtggtggtga ccggggcgtc gggtttcgtc gggtcatggc 180
tcgtcatgaa gctccttcag gcggggtaca ccgtccgggc caccgtgcgc gaccctggga 240
acgtcgagaa gacgaagcca ttgctggagc ttcccggagc caaggagcgg ctgtccatct 300
ggcgtgccga cctgagcgag gaaggcagct tcgacgaggc catcgcgggc tgcaccggcg 360
tcttccacgt cgccacgccc atggacttcg agtccaagga ccctgagaac gaagtgatca 420
agccgacggt ggaagggatg ctgagcatca tgagagcgtg caaggaggcc ggcaccgtca 480
agcgcgtcgt cttcacctcc tccgccggca ccgtcaacat tgaggagcgg ccgaggccgg 540
cctacgacca ggacaactgg agcgacatcg acttctgccg ccgcgtcaag atgacaggac 600
agatgtactt cgtgtccaag tccctggcgg agaaggccgc catggactac gccaaggaga 660
acggcgtgga cttcatcagc atcatcccca cgctcgtcgt cggcccctt ctcagcgccg 720
gcatgccgcc cagcctggtc accgccctgg cactcatcac ggggaacgag gcccactact 780
cgatcctgaa gcaggtgcag ctggtccacc tggacgacct ctgcgactcc atgacctacc 840
tcttcgagca cccggacgcc aacggccgct acatctgctc ctcccacgac accaccattc 900
atggcatcgc caggatgctc aaggagaggt tccccgagta cgacatccca cagaaattcc 960
cgggagtcga cgacgacctc cagccgatcc acttcttctt caagaagctg ctcgaccacg 1020
ggttcaggtt caggtacacc gccgaggaca tgttcgacgc cgcggtctgg acgtgcaggg 1080
agaagggcct gattccgctc ggagcggaag ggcaggcgg cccggccagt gcagccggca 1140
agctgggagc tgttctcgtg ggcgaaggtc aggcgattgg tgctgagaca taagcgctag 1200
tgcatgtaca ctaggctggc tacctcagac acatggtgga gcgatgatta tgttcgttaa 1260
ttctactatc ctatatttcg gttcagaaat tgcattaaga gaaccctgta attggtggga 1320
tattatgaac ggattatgga acgcaaataa cttcatgaca aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1418

<210> 159
<211> 1209
<212> DNA
<213> Lolium perenne

<400> 159
gagcaccaca catggcgact gaagccaagg gggagacggt gctggtcacc ggcgccagcg 60
gcttcatcgg ctcctggctc gtccgcctcc tcctcgcccg cggctactcc gtccacgccg 120
ccgtcctcaa ccccgatgac aaggccgaga cggaccacct cctcgcgctc gccgctgcgg 180
ccggcgacga gggccgcatc cgcttcttca ggtgcgacct cctcgacggc gccgccatgc 240
tcgccgccgt gcggggatgc tccggcgtgt tccacctcgc ctctccctgc accgtcgacc 300
tcgtcctcga cccccagaag gagcttgtgg tgccggcggt ggagggcacg ctcaacgtgc 360
tgcgcgccgc caaggaagct gggggagtgc ggcgggtggt ggtgacctcc tccgtctccg 420
ccctcgtccc ctgcccgggg tggccggccg gcgaggtcct cgacgagcgc tgctggaccg 480
acatcgacta ctgcgacaag aacggggttt ggtaccctgc ttcaaaggca ctggcggaga 540
aggcggcatg gaagtttgca gaggagaatg gactggatgt ggtgacggtc aatccaggga 600
cggttttggg cgagatgatt ccgccaaggc tcaatgccag catggccatg tttcttcgct 660
tacttgaagg ttgcaaagag gagtatgcag atttcttcat cgggccagtg cacgtggaag 720
acgttgcatt agcccatatt ctgctgtacg agaatccgtc agcatccggg aggcacctct 780
gcgtggagcc catctgtcac tggagtgttt tcgcggcgaa agtcgccgag ctctaccctg 840
attacaaagt tccaaaattc cctgaggaca cacagcctgg gctggtgagg gcggaggcgg 900
tgccaaagaa gctgatggcg ttgggtttgc agttcactcc tcttgagaag atcatcaggg 960
atgccgtgga gagcctcaag agcagaggat gcatcgcctg atgattggat cgttaggcat 1020
gtcacccttc cgtcgtaggt tcatgatcat ccttgttgag agatgtgttg tgttgtgtcc 1080
agcccagtgc ctacccagac catatactta ccagtatgat ttgtgcaata acagccggtt 1140
gatgtacggc atcacctgcc ctacacttgg gatgcggatg ctgtcacact gactccctca 1200
aaaaaaaaa 1209

<210> 160
<211> 1260
<212> DNA
<213> Lolium perenne

<400> 160
gaaaagcttc acacagcttg agaaaatggt gagctcaacc aagggcaaag tgtgtgtaac 60
tggggcttca ggctttgttg cctcttggct catcaagaaa ctccttgagt ctggatatca 120
tgtgataggg actgtcagag acccagggaa tcgaagaaag gtgggacacc tttggaaact 180
accaggtgca aatgagaggc tccaacttgt gagagctgat ctattggagg aagggagctt 240
tgacgatgct gtaagggctt gtgagggtgt cttccacatt gcgtcgcctg tccttgggaa 300
atctgattcc aattgcaagg aagcaacact cggtcctgca atcaatggta ccctcaacgt 360

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gctaagatcc tgcaagaaga gtccatttct caaaagggtt gttctcacat cttcatcatc     420
cgcggtaagg attagggatg aaactcagca gccagaactg ttatgggatg aaacgacatg     480
gagctctgtg ccactctgtg aaaagctaca gctatggtat gccctggcaa aggtatttgc     540
agagaaagca gcattggact ttgccaagga gaataacatt gaccttgtga cagttcttcc     600
atcattcgta attggaccca gtttatccca tgaattgtgc actactgctt cagatatcct     660
tggcttactt caaggtgaca cagacaggtt cactttgtac ggaaggatgg gatatgttca     720
catcgatgat gttgcccgga gccacattct agtgtacgaa acaccggagg caactggcag     780
atatctgtgc agctcagtgg ttctggataa caatgaattg gttggcttac tggcaaaaca     840
gtttccagta ttccccattc caaggaggct caagaacccc tatggaaagc aggcatacca     900
gctagacaca tccaagctcc aggggctggg tctcaagttc aaaggagtgc aggagatgtt     960
taacgactgc gtcgaatcgc tgaaagatca gggccatttg ctggagtgcc cgttgtgata    1020
acagagacag cattgacaag ccatagccaa acagcattga caagccatag ccaaacacat    1080
ctcaactatg cctgaatcat gtcagttctc gagtcataga ttttttttt ctcttcaaat     1140
aattcccatg tactctcctt actataccga acatcaattg tcagcggcag attaaatgtg    1200
tccatatgct ttgcaattgt ttcaattagt aatgaaatat ttgaaacaaa aaaaaaaaa     1260
```

<210> 161
<211> 1438
<212> DNA
<213> Lolium perenne

<400> 161

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aaacgactcc aacgcaccga tcgacgacac accctgcact tcacgggtcg atcggatcgg      60
aggatggcgc cggtggtgga gagagcgccc ttcctgccga cgggggaggc cacgctgcgg     120
ccgtccttcg tgcgggacga ggacgagcgg cccaaggtgg cgcacgaccg cttcagcgac     180
gaggtgcccg tcatctcgct ccacggcatc gacgacgcgc ggaggaccga gatccgggac     240
cgcgtggcgg cggcgtgcga ggggtggggc atcttccagg tcgtcgacca cggcgtcgac     300
gccgcgctca tcgccgagat ggccaggctc tcgcgcgact tcttcgcgct ccccgccgag     360
gacaagctcc gctacgacat gtccggcggc aagaagggcg gattcatcgt ctccagccac     420
ctccagggcg agacggtcca ggactggcgg gagatcgtga cctacttctc gtacccggtc     480
aaggcgcggg actacggccg gtggccggac aagcccgcgg ggtggcgcgc ggtggtggag     540
cagtacagcg agcggctcat ggcgctgtcc tgcaagctgc tgggggtgct gtcggaggcc     600
atgggcctgg agacggaggc cctgtccaag gcgtgcgtgg acatggacca gaaggtggtg     660
gtcaacttct accccaagtg cccccagccc gacctcaccc tcggcctcaa gcgccacacc     720
gaccccggca ccatcaccct cctcctccag gacctcgtcg gcggactcca ggccacccgc     780
gacggcggca acacctggat caccgtacag cccatcgccg gcgcattcgt cgtcaacctc     840
ggcgaccacg gccactactt gagcaacggg aggtttaaga acgcggacca ccaggcggtg     900
gtgaacgggg agagcagcag gctgtccatc gccacgttcc agaacccggc gcccgacgcc     960
aaggtgtggc cgctggcggt gagggagggg gaggacacca tcctggagga gcccatcacc    1020
ttcaccgaga tgtaccgccg caagatggcg cgcgacctcg agctcgccaa gcgcaagaag    1080
caggccaagg ccgatcagct caagcagcag ctgcagcagg aggccgcgcc cgccgccgcg    1140
cccaccaagc cactcaacca gattcttgcc tagattccat gccgattcat tcatgcgtga    1200
tatatagtac tatgtactat atcgtattaa aataagtaat tatctctatc tactcatttg    1260
tgtgtaatta agagatgagt aattatctag tatatacaca tttgtctgcg aggagcgagc    1320
tggacctgta ataacatgta gcatgtccta cgtggaaccg atcagctgat tggagctgtc    1380
acatgagttt gctgtgtgca gaaattgaac gcattcggta ctgctttcaa aaaaaaaa      1438
```

<210> 162
<211> 1214
<212> DNA
<213> Lolium perenne

<400> 162

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gaaaatcccc aaacccaaaa ggtgaggcct ccagatactt ggatctccaa tggctcctgc      60
tactcccaag gacagctcta gctctgctct gcctggtttg ctcttgctcc tcgcagcagc     120
gacgtccgtg gcggtagcga acgcacagct atcagagaac tactacgggt cttcttgtcc     180
caccgcgctt ctcaccatca ggactgtcgt gacgacggcg gtgctgctgg accaccgcat     240
gggcgcttct cttctccggc tccacttcca cgactgcttt gtgcaagggt gcgacgcgtc     300
cgttctgctg gatgacacgg ccggcttcac cggcgagaag ggggccgggc cgaacgccgg     360
gtcgctgcgc ggtctggagg tgatcgacaa gatcaagatg ctgctggagt tcatgtgccc     420
gcggaccgtc tcctgcgccg acatcctcgc cgtcgccgcc cgcgactccg tcgtccgtct     480
agggggggcca tcatgggcgg ttcaacttgg aaggagggac gccaccacag caagcgcgtc     540
acttgctagt agtgacctcc caggccccaa ctccaacctc aatgatctcc tcaccgcttt     600
ctccaaaaaa ggactaagca ccacggacat ggttgctcta tcaggggccc ataccatcgg     660
ccgggcgcag tgccagaact accggaaccg gatctacacc gacaccgaca ttgacggggc     720
attcgcagcg tccctgcgag gcggctgccc acaggccggc ggcgacggca acctcgcgcc     780
```

gctcgacgcg tcctctccca acaccttcga taacggctac ttctccggcc tcctctcccg 840
ccaggggctg ctccattccg accaggcgct gtacgacggc ggctccacgg acgatctggt 900
caggacctac gcctccaata acgatcagtt tggcagcgac ttcgctgcgg cgatggtgaa 960
actgagcaat atcggcctgc tgacggggtc gtccggggag atcagggtca actgccgggc 1020
ggtgaattaa cgatggatgg atgggggcat catgaaacga acaaggcgtg cgatttccgg 1080
aactgcaggc aacgaaactg catatttatg tacactgcct atttatttcc tgtccttgtg 1140
tccccgtctt gttatattac atccataatc catgttaaga tggtggcatt ggtttaaaaa 1200
aaaaaaaaaa aaaa 1214

<210> 163
<211> 654
<212> PRT
<213> Lolium perenne

<400> 163
Met Glu Ser Ser Ala Val Val Pro Gly Thr Thr Ala Pro Leu Leu Pro
1 5 10 15
Tyr Ala Tyr Ala Pro Leu Pro Ser Ser Ser Asp Asp Ala Arg Glu Asn
20 25 30
Arg Ser Ser Gly Gly Val Arg Trp Arg Ala Cys Ala Ala Val Leu Ala
35 40 45
Ala Ser Ala Leu Ala Val Val Val Val Val Gly Leu Leu Ala Gly Gly
50 55 60
Arg Val Asp Arg Val Pro Ala Gly Ala Asp Val Ala Ser Ala Thr Val
65 70 75 80
Pro Ala Val Pro Met Glu Phe Pro Arg Ser Arg Gly Lys Asp Leu Gly
85 90 95
Val Ser Glu Lys Ser Ser Gly Ala Tyr Ser Ala Asp Gly Gly Phe Pro
100 105 110
Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe His Phe Gln
115 120 125
Pro Glu Gln His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly
130 135 140
Gly Trp Tyr His Leu Phe Tyr Gln His Asn Pro Lys Gly Asp Ser Trp
145 150 155 160
Gly Asn Ile Ala Trp Ala His Ala Val Ser Lys Asp Met Val Asn Trp
165 170 175
Arg His Leu Pro Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ser Asn
180 185 190
Gly Val Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Gln Val Ile
195 200 205
Leu Leu Tyr Thr Gly Asn Thr Asp Thr Leu Ala Gln Val Gln Cys Leu
210 215 220
Ala Thr Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Glu Trp Ile Lys
225 230 235 240
His Pro Ala Asn Pro Ile Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys
245 250 255
Asp Phe Arg Asp Pro Leu Thr Ala Trp Phe Asp His Ser Asp His Thr
260 265 270
Trp Arg Thr Val Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile
275 280 285
Ile Leu Ser Tyr Lys Thr Lys Asp Phe Val Asn Tyr Glu Leu Met Pro
290 295 300
Gly Asn Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Ile
305 310 315 320
Asp Leu Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp
325 330 335
Asp Ser Pro Asp Val Leu Phe Val Leu Lys Glu Ser Ser Asp Asp Glu
340 345 350
Arg His Asp Tyr Tyr Ala Leu Gly Arg Phe Asp Ala Val Ala Asn Val
355 360 365
Trp Thr Pro Ile Asp Arg Asp Leu Asp Leu Gly Ile Gly Leu Arg Tyr
370 375 380
Asp Trp Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Gln Lys Lys
385 390 395 400

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Asn Arg Arg Ile Val Trp Ala Tyr Ile Gly Glu Thr Asp Ser Glu Gln
                405                 410                 415
Ala Asp Ile Thr Lys Gly Trp Ala Asn Leu Met Thr Ile Pro Arg Thr
            420                 425                 430
Val Glu Leu Asp Arg Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val
        435                 440                 445
Glu Glu Val Asp Thr Leu Arg Arg Asn Ser Thr Asp Leu Gly Arg Ile
    450                 455                 460
Thr Val Asn Ala Gly Ser Val Ile Arg Leu Pro Leu His Gln Gly Ala
465                 470                 475                 480
Gln Leu Asp Ile Glu Ala Ser Phe Gln Leu Asn Ser Ser Asp Val Asp
                485                 490                 495
Ala Ile Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr Ser Gly Ala
            500                 505                 510
Ala Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Leu Ala Asn
        515                 520                 525
Gly Arg Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Lys Gly Val
    530                 535                 540
Asp Gly Gly Leu Gln Thr His Phe Cys His Asp Glu Ser Arg Ser Thr
545                 550                 555                 560
Arg Ala Lys Asp Val Val Asn Arg Met Ile Gly Ser Ile Val Pro Val
                565                 570                 575
Leu Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile
            580                 585                 590
Val Gln Ser Phe Ala Met Gly Gly Arg Ile Thr Ala Thr Ser Arg Ala
        595                 600                 605
Tyr Pro Thr Glu Ala Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn
    610                 615                 620
Asn Ala Thr Gly Ala Thr Val Thr Ala Glu Arg Leu Val Val His Glu
625                 630                 635                 640
Met Ala Ser Ala Asp Asn His Ile Phe Thr Asn Asp Asp Leu
                645                 650

<210> 164
<211> 620
<212> PRT
<213> Festuca arundinacea

<400> 164
Met Glu Ser Arg Ala Phe Pro Asn Ala Ala Tyr Ala Pro Leu Leu Pro
 1               5                  10                  15
Pro Thr Ala Asp Asp Ala Thr Leu Gly Lys Gln Asp Arg Pro Gly Val
            20                  25                  30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Ser Gly Val Val Val
        35                  40                  45
Leu Leu Val Ala Ala Thr Met Leu Ala Gly Ser Arg Met Gly Gln Ala
    50                  55                  60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
65                  70                  75                  80
Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
                85                  90                  95
Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
            100                 105                 110
Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
        115                 120                 125
Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
    130                 135                 140
Pro Leu Ala Leu Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
145                 150                 155                 160
Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
                165                 170                 175
Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
            180                 185                 190
Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
        195                 200                 205
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Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
    210                 215                 220
Arg Asp Pro Thr Ser Ala Trp Phe Asp Lys Ser Asp Ala Thr Trp Arg
225                 230                 235                 240
Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
                245                 250                 255
Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
            260                 265                 270
Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
        275                 280                 285
Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
    290                 295                 300
Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
305                 310                 315                 320
Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
                325                 330                 335
Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
            340                 345                 350
Ala Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
        355                 360                 365
Tyr Val Gly Glu Thr Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
    370                 375                 380
Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Thr Leu Asp Glu Lys Thr
385                 390                 395                 400
Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
                405                 410                 415
Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Asp Asn Gly Ser Val
            420                 425                 430
Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
        435                 440                 445
Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
    450                 455                 460
Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala Arg Gly Ala Ile
465                 470                 475                 480
Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
                485                 490                 495
Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Thr Leu
            500                 505                 510
Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
        515                 520                 525
Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu His Gly Glu
    530                 535                 540
Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
545                 550                 555                 560
Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
                565                 570                 575
Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
            580                 585                 590
Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
        595                 600                 605
Val Tyr Asp Glu Thr Leu Ile Met Val Glu Asp Ser
    610                 615                 620
```

<210> 165
<211> 623
<212> PRT
<213> Festuca arundinacea

<400> 165

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Met Glu Ser Arg Ala Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
1               5                   10                  15
Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
            20                  25                  30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
        35                  40                  45
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Leu Leu Val Gly Ala Thr Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
    50                  55                  60
Gly Asp Gly Glu Gly Asn Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro
65                  70                  75                  80
Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln
                85                  90                  95
Pro Glu Gly His Phe Met Ser Asp Pro Asn Gly Pro Val Tyr Tyr Arg
            100                 105                 110
Gly Tyr Tyr His Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp
        115                 120                 125
Asp Asp Tyr Ile Glu Trp Gly His Val Val Ser Gln Asp Leu Val His
    130                 135                 140
Trp Arg Pro Leu Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys
145                 150                 155                 160
Lys Gly Val Leu Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu
                165                 170                 175
Val Leu Leu Tyr Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln
            180                 185                 190
Cys Ile Ala Val Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp
        195                 200                 205
Thr Lys His Pro Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln
    210                 215                 220
Gly Met Asp Phe Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp
225                 230                 235                 240
Ala Thr Trp Arg Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser
                245                 250                 255
His Ala Gly Ile Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe
            260                 265                 270
Glu Arg Val Pro Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp
        275                 280                 285
Glu Cys Ile Asp Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser
    290                 295                 300
Glu Glu Leu Tyr Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp
305                 310                 315                 320
Tyr Tyr Ser Leu Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro
                325                 330                 335
Leu Asp Ala Glu Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly
            340                 345                 350
Lys Leu Tyr Ala Ser Thr Ser Phe Tyr Asp Pro Val Lys Gln Arg Arg
        355                 360                 365
Ile Met Leu Gly Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val
    370                 375                 380
Ala Lys Gly Trp Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu
385                 390                 395                 400
Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val
                405                 410                 415
Glu Ala Leu Arg Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Ile Asp
            420                 425                 430
Asn Gly Ser Val Phe His Leu Pro Leu His Gln Thr Thr Gln Leu Asp
        435                 440                 445
Ile Glu Ala Ser Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn
    450                 455                 460
Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala
465                 470                 475                 480
Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp
                485                 490                 495
Leu Arg Gly Glu Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu
            500                 505                 510
Asp Gly Thr Leu Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser
        515                 520                 525
Arg Ala Arg Asp Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val
    530                 535                 540
Leu Asp Gly Glu Ala Leu Ser Met Arg Val Leu Val Asp His Ser Ile
545                 550                 555                 560
Val Gln Ser Phe Ala Met Gly Gly Arg Thr Thr Ala Thr Ser Arg Val
                565                 570                 575
```

Tyr Pro Thr Glu Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn
580 585 590
Asn Ala Thr Gly Ala Gly Val Thr Ala Glu Arg Leu Ile Val His Glu
595 600 605
Met Ala Ser Ala Val Tyr Asp Glu Thr Leu Met Val Glu Asp Ser
610 615 620

<210> 166
<211> 619
<212> PRT
<213> Festuca arundinacea

<400> 166
Met Glu Ser Arg Asp Phe Pro Ser Ala Ala Tyr Ala Pro Leu Leu Pro
1 5 10 15
Ser Ala Ala Asp Asp Val Ala Leu Ala Lys Gln Asp Arg Pro Gly Val
20 25 30
Gly Trp Arg Gly Phe Leu Thr Val Leu Ala Ala Cys Gly Val Val Val
35 40 45
Leu Leu Val Ala Ala Ser Leu Leu Ala Gly Ser Arg Met Gly Gln Ala
50 55 60
Gly Asp Thr Asp Glu Asp Gly Ala Gly Gly Phe Pro Trp Ser Asn Glu
65 70 75 80
Met Leu Gln Trp Gln Arg Ala Gly Phe His Tyr Gln Pro Glu Gly His
85 90 95
Phe Met Ser Asp Pro Asp Gly Pro Val Tyr Tyr Arg Gly Tyr Tyr His
100 105 110
Leu Phe Phe Gln Tyr Asn Arg Arg Gly Val Ala Trp Asp Asp Tyr Ile
115 120 125
Glu Trp Gly His Val Val Ser Gln Asp Leu Val His Trp Arg Pro Leu
130 135 140
Pro Leu Ala Met Arg Pro Asp His Trp Tyr Asp Lys Lys Gly Val Leu
145 150 155 160
Ser Gly Thr Ile Thr Val Leu His Asn Gly Thr Leu Val Leu Leu Tyr
165 170 175
Thr Gly Val Thr Glu Asp Pro Met Ala Glu Ser Gln Cys Ile Ala Val
180 185 190
Pro Thr Asp Pro Asn Asp Pro Leu Leu Arg His Trp Thr Lys His Pro
195 200 205
Ala Asn Pro Val Leu Ala His Pro Gln Gly Val Gln Gly Met Asp Phe
210 215 220
Arg Asp Pro Thr Ser Ala Trp Trp Asp Lys Ser Asp Ser Thr Trp Arg
225 230 235 240
Ile Leu Ile Gly Ser Lys Asp Asp Asp Asn Gly Ser His Ala Gly Ile
245 250 255
Ala Phe Ile Phe Lys Thr Lys Asp Phe Leu Ser Phe Glu Arg Val Pro
260 265 270
Gly Ile Val His Arg Val Glu Gly Thr Gly Met Trp Glu Cys Ile Asp
275 280 285
Phe Tyr Pro Val Gly Gly Gly His Asn Ser Ser Ser Glu Glu Leu Tyr
290 295 300
Val Ile Lys Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu
305 310 315 320
Gly Arg Tyr Asp Ala Ala Ala Asn Thr Trp Thr Pro Leu Asp Ala Glu
325 330 335
Leu Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Leu Tyr Ala
340 345 350
Ser Thr Ser Phe Tyr Asp Pro Leu Lys Gln Arg Arg Ile Met Leu Gly
355 360 365
Tyr Val Gly Glu Val Asp Ser Ala Arg Ala Asp Val Ala Lys Gly Trp
370 375 380
Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Ala Leu Asp Glu Lys Thr
385 390 395 400
Arg Thr Asn Leu Leu Leu Trp Pro Val Glu Glu Val Glu Ala Leu Arg
405 410 415

```
Tyr Asn Ser Thr Asp Leu Ser Gly Ile Thr Val Glu Asn Gly Ser Ile
            420                 425                 430
Phe His Leu Pro Leu His Gln Ala Thr Gln Leu Asp Ile Glu Ala Ser
        435                 440                 445
Phe Arg Leu Asp Ala Ser Asp Val Ala Ala Ile Asn Glu Ala Asp Val
    450                 455                 460
Gly Tyr Asn Cys Ser Ser Ser Gly Gly Ala Ala Ala Arg Gly Ala Leu
465                 470                 475                 480
Gly Pro Phe Gly Leu Leu Val His Ala Ala Gly Asp Leu Arg Gly Glu
                485                 490                 495
Gln Thr Ala Val Tyr Phe Tyr Val Ser Arg Ala Leu Asp Gly Ser Leu
            500                 505                 510
Arg Thr Ser Phe Cys Asn Asp Glu Thr Arg Ser Ser Arg Ala Arg Asp
        515                 520                 525
Val Thr Lys Arg Val Val Gly Ser Thr Val Pro Val Leu Asp Gly Glu
    530                 535                 540
Val Leu Ala Met Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe
545                 550                 555                 560
Ala Met Gly Gly Arg Val Thr Ala Thr Ser Arg Val Tyr Pro Thr Glu
                565                 570                 575
Ala Ile Tyr Ala Arg Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Gly
            580                 585                 590
Ala Ser Val Thr Ala Glu Arg Leu Ile Val His Glu Met Ala Ser Ala
        595                 600                 605
Val Tyr Asp Glu Thr Val Met Val Lys Asp Ser
    610                 615
```

<210> 167
<211> 1075
<212> PRT
<213> Lolium perenne

<400> 167

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Met Ala Gly Asn Asp Trp Ile Asn Ser Tyr Leu Glu Ala Ile Leu Asp
 1               5                  10                  15
Ala Gly Gly Thr Ala Gly Asp Ile Ser Ala Ala Ser Val Ala Gly Gly
            20                  25                  30
Asp Asp Gly Pro Gly Ala Gly Gly Gly Thr Ala Gly Glu Lys Arg Asp
        35                  40                  45
Lys Ser Ser Leu Met Leu Arg Glu Arg Gly Arg Phe Asn Pro Ala Arg
    50                  55                  60
Tyr Phe Val Glu Glu Val Ile Ser Gly Phe Asp Glu Thr Asp Leu Tyr
65                  70                  75                  80
Lys Thr Trp Val Arg Thr Ser Ala Met Arg Ser Pro Gln Glu Arg Asn
                85                  90                  95
Thr Arg Leu Glu Asn Met Ser Trp Arg Ile Trp Asn Leu Ala Arg Lys
            100                 105                 110
Lys Lys Gln Ile Glu Gly Glu Glu Ala Ser Arg Leu Ser Lys Lys Arg
        115                 120                 125
Leu Glu Arg Glu Lys Ala Arg Arg Asp Ala Ala Ala Asp Leu Ser Glu
    130                 135                 140
Asp Leu Ser Glu Gly Glu Lys Gly Glu Asn Ile Asn Gly Ser Ser Val
145                 150                 155                 160
His Asp Glu Ser Thr Arg Gly Arg Met Pro Arg Ile Gly Ser Thr Asp
                165                 170                 175
Ala Ile Glu Val Trp Ala Asn Gln His Lys Asp Lys Lys Leu Tyr Ile
            180                 185                 190
Val Leu Ile Ser Ile His Gly Leu Ile Arg Gly Glu Asn Met Glu Leu
        195                 200                 205
Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
    210                 215                 220
Ala Arg Ala Leu Gly Glu Thr Pro Gly Val Tyr Arg Val Asp Leu Leu
225                 230                 235                 240
Thr Arg Gln Ile Ser Ala Pro Asp Val Asp Trp Ser Tyr Gly Glu Pro
                245                 250                 255
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Thr Glu Met Leu Ser Pro Arg Asn Ser Glu Asn Leu Gly Asp Asp Met
            260                 265                 270
Gly Glu Ser Ser Gly Ala Tyr Ile Val Arg Ile Pro Phe Gly Pro Arg
        275                 280                 285
Glu Lys Tyr Ile Pro Lys Glu Gln Leu Trp Pro His Ile Gln Glu Phe
    290                 295                 300
Val Asp Gly Ala Leu Val His Ile Met Gln Met Ser Lys Val Leu Gly
305                 310                 315                 320
Glu Gln Val Gly Arg Glu Arg Arg Val Trp Pro Val Val Ile His Gly
                325                 330                 335
His Tyr Ala Asp Ala Gly Asp Ser Ala Ala Leu Leu Ser Gly Ala Leu
            340                 345                 350
Asn Val Pro Met Val Phe Thr Gly His Ser Leu Gly Arg Asp Lys Leu
        355                 360                 365
Glu Gln Leu Leu Lys Gln Gly Arg Gln Thr Arg Asp Glu Val Asn Ala
    370                 375                 380
Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Cys Leu Asp
385                 390                 395                 400
Ala Ser Glu Ile Val Ile Thr Ser Thr Arg Gln Glu Ile Glu Lys Gln
                405                 410                 415
Trp Gly Leu Tyr Asn Gly Phe Asp Val Thr Met Glu Arg Lys Leu Arg
            420                 425                 430
Ala Arg Thr Lys Arg Gly Val Ser Cys Tyr Gly Arg Tyr Met Pro Arg
        435                 440                 445
Met Ile Ala Ile Pro Pro Gly Met Glu Phe Ser His Ile Val Pro His
    450                 455                 460
Asp Val Asp Leu Asp Gly Asp Glu Ala Asn Glu Val Gly Ser Gly Ser
465                 470                 475                 480
Pro Asp Pro Pro Ile Trp Ala Asp Ile Met Arg Phe Phe Ser Asn Pro
                485                 490                 495
Arg Lys Pro Met Ile Leu Ala Leu Ala Arg Pro Asp Pro Lys Lys Asn
            500                 505                 510
Ile Thr Thr Leu Val Lys Ala Phe Gly Glu His Pro Gly Leu Arg Asn
        515                 520                 525
Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Asp Val Ile Asp Glu
    530                 535                 540
Met Ser Ser Thr Asn Gly Ala Val Leu Thr Ser Val Leu Lys Leu Ile
545                 550                 555                 560
Asp Lys Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
                565                 570                 575
Gln Ser Glu Val Pro Asp Ile Tyr Arg Leu Ala Ala Arg Thr Lys Gly
            580                 585                 590
Val Phe Ile Asn Cys Ala Tyr Ile Glu Pro Phe Gly Leu Thr Leu Ile
        595                 600                 605
Glu Ala Ala Ala Tyr Gly Leu Pro Met Val Ala Thr Gln Asn Gly Gly
    610                 615                 620
Pro Val Asp Ile His Arg Val Leu Asp Asn Gly Ile Leu Val Asp Pro
625                 630                 635                 640
His Asn Gln Asn Asp Ile Ala Glu Ala Leu Tyr Lys Leu Val Ser Asp
                645                 650                 655
Lys His Leu Trp Ala Gln Cys Arg Gln Asn Gly Leu Asp Asn Ile His
            660                 665                 670
Arg Phe Ser Trp Pro Glu His Cys Lys Asn Tyr Leu Ser Arg Val Gly
        675                 680                 685
Thr Val Lys Pro Arg His Pro Arg Trp Gln Arg Ser Asp Asp Ala Thr
    690                 695                 700
Glu Val Ser Glu Ser Asp Ser Pro Gly Asp Ser Leu Arg Asp Val His
705                 710                 715                 720
Asp Ile Ser Leu Asn Leu Lys Leu Ser Leu Asp Ser Glu Lys Ala Gly
                725                 730                 735
Thr Lys Ile Asn Thr Glu Arg Asn Ser Thr Asn Ala Arg Arg Asn Leu
            740                 745                 750
Glu Asp Ala Val Leu Lys Phe Ser Asn Ala Val Ser Glu Gly Thr Lys
        755                 760                 765
Asp Glu Ser Asp Glu Asn Ala Glu Ala Thr Thr Gly Ser Asn Lys Trp
    770                 775                 780
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Pro Ser Leu Arg Arg Arg Lys His Ile Val Val Ile Ala Val Asp Ser
785 790 795 800
Val Gln Asn Ala Asp Leu Val Gln Ile Ile Lys Asn Leu Phe Glu Ala
805 810 815
Ser Arg Lys Glu Lys Ser Ser Gly Ala Val Gly Phe Val Leu Ser Thr
820 825 830
Ser Arg Ala Ile Ser Glu Thr Leu Thr Phe Leu Thr Ser Gly Gly Ile
835 840 845
Gln Thr Thr Glu Phe Asp Ala Phe Ile Cys Ser Ser Gly Ser Asp Leu
850 855 860
Cys Tyr Pro Ser Ser Ser Ser Glu Asp Met Leu Ser Pro Thr Glu Leu
865 870 875 880
Pro Phe Met Ile Asp Leu Asp Tyr His Ser Gln Ile Glu Tyr Arg Trp
885 890 895
Gly Gly Glu Gly Leu Arg Lys Thr Leu Ile Arg Trp Ala Ala Glu Asn
900 905 910
Asn Ser Gln Ser Gly Gln Glu Val Val Thr Glu Asp Glu Glu Cys Ser
915 920 925
Ser Thr Tyr Cys Ile Ser Phe Lys Val Lys Asn Thr Glu Ala Val Pro
930 935 940
Pro Val Lys Asp Leu Arg Lys Thr Met Arg Ile Gln Ala Leu Arg Cys
945 950 955 960
His Val Leu Tyr Ser His Asp Gly Ser Lys Leu Asn Leu Ile Pro Leu
965 970 975
Leu Ala Ser Arg Ser Gln Ala Leu Arg Tyr Leu Tyr Ile Arg Trp Gly
980 985 990
Val Glu Leu Ala Asn Met Thr Val Val Val Gly Glu Ser Gly Asp Thr
995 1000 1005
Asp Tyr Glu Gly Leu Leu Gly Gly Val His Lys Thr Ile Ile Leu Lys
1010 1015 1020
Gly Ser Phe Asn Ala Ala Pro Asn Gln Leu His Ala Ala Arg Ser Tyr
1025 1030 1035 1040
Ser Leu Glu Asp Val Ile Ser Phe Asp Lys Pro Gly Ile Ala Ser Val
1045 1050 1055
Glu Gly Tyr Leu Pro Asp Ser Leu Lys Ser Ala Leu Gln Gln Phe Gly
1060 1065 1070
Val Leu Asn
1075

<210> 168
<211> 938
<212> PRT
<213> Lolium perenne

<400> 168
Met Ala Ala Gly Asn Glu Trp Ile Asn Gly Tyr Leu Glu Ala Ile Leu
1 5 10 15
Asp Ala Gly Ser Lys Leu Arg Pro Gln Gly Val Gln Leu Pro Pro Leu
20 25 30
Glu Thr Ala Pro Ala Leu Ala Ala Glu Glu Ser Ser Ala Ala Tyr Asn
35 40 45
Pro Thr Arg Tyr Phe Val Glu Glu Val Val Arg Ser Phe Asp Glu Gln
50 55 60
Ala Leu His Lys Thr Trp Thr Lys Val Val Ala Met Arg Asn Ser Gln
65 70 75 80
Glu Arg Ser Asn Arg Leu Glu Asn Leu Cys Trp Arg Ile Trp Asn Val
85 90 95
Ser Arg Gln Lys Lys Gln Val Glu Trp Asp Tyr Thr Lys Glu Val Ala
100 105 110
Arg Arg Lys Leu Glu Gln Glu Leu Gly Ser Arg Glu Ala Ala Glu Asp
115 120 125
Leu Ser Glu Leu Ser Glu Gly Glu Lys Asp Thr Thr Thr Ala Lys Pro
130 135 140
Asp Ala Ala Ala Ala Gln Pro Ser Ala Asp Asp Gly Glu His Gln Gln
145 150 155 160

```
Pro Gln Pro Arg Thr Arg Leu Ala Arg Ile Asn Ser Glu Val Arg Leu
                165                 170                 175
Val Ser Asp Asp Glu Glu Glu Gln Thr Lys Lys Arg Asn Leu Tyr Ile
            180                 185                 190
Val Leu Ile Ser Ile His Gly Leu Val Arg Gly Glu Asn Met Glu Leu
        195                 200                 205
Gly Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Leu
    210                 215                 220
Ala Arg Ala Leu Ala Ala Thr Ala Gly Val His Arg Val Asp Leu Leu
225                 230                 235                 240
Thr Arg Gln Ile Ser Cys Pro Asp Val Asp Trp Thr Tyr Gly Glu Pro
                245                 250                 255
Val Glu Met Leu Glu Arg Leu Ser Ser Ala Asp Ala Asp Asp Asp Asp
            260                 265                 270
Gly Glu Gln Ala Gly Gly Gly Ala Tyr Ile Val Arg Leu Pro Cys Gly
        275                 280                 285
Pro Arg Asp Gln Tyr Ile Pro Lys Glu Glu Leu Trp Pro His Ile Pro
    290                 295                 300
Glu Phe Val Asp Arg Ala Leu Ser His Val Thr Glu Val Ala Arg Ala
305                 310                 315                 320
Leu Gly Glu Gln Leu Gln Pro Pro Pro Ser Pro Ala Asp Gly Ala Val
                325                 330                 335
Ala Ala Pro Ile Trp Pro Tyr Val Ile His Gly His Tyr Ala Asp Ala
            340                 345                 350
Ala Glu Val Ala Ala Asn Leu Ala Ser Ala Leu Asn Val Pro Met Val
        355                 360                 365
Met Thr Gly His Ser Leu Gly Arg Asn Lys Leu Glu Gln Leu Leu Lys
    370                 375                 380
Leu Gly Arg Met Pro Gly Pro Glu Ile Gln Gly Thr Tyr Lys Ile Ala
385                 390                 395                 400
Arg Arg Ile Glu Ala Glu Glu Thr Gly Leu Asp Thr Ala Glu Met Val
                405                 410                 415
Val Thr Ser Thr Lys Gln Glu Ile Glu Glu Gln Trp Gly Leu Tyr Asp
            420                 425                 430
Gly Phe Asp Leu Met Val Glu Arg Lys Leu Arg Val Arg Gln Arg Arg
        435                 440                 445
Gly Val Ser Ser Leu Gly Arg Tyr Met Pro Arg Met Ala Val Ile Pro
    450                 455                 460
Pro Gly Met Asp Phe Ser Phe Val Glu Thr Gln Asp Thr Ala Asp Gly
465                 470                 475                 480
Asp Gly Ala Asp Leu Gln Met Leu Ile Ala Pro Asp Lys Ala Lys Lys
                485                 490                 495
Ala Leu Pro Pro Ile Trp Ser Asp Val Leu Arg Phe Phe Thr Asn Pro
            500                 505                 510
His Lys Pro Met Ile Leu Ala Leu Ser Arg Pro Asp Pro Lys Lys Asn
        515                 520                 525
Val Thr Thr Leu Leu Lys Ala Tyr Gly Glu Ser Arg Gln Leu Arg Glu
    530                 535                 540
Leu Ala Asn Leu Thr Leu Ile Leu Gly Asn Arg Asp Asp Ile Glu Asp
545                 550                 555                 560
Met Ala Gly Gly Gly Gly Ala Val Leu Thr Ala Val Leu Lys Leu Ile
                565                 570                 575
Asp Arg Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys
            580                 585                 590
Gln Thr Asp Val Pro His Ile Tyr Arg Leu Ala Ala Lys Thr Lys Gly
        595                 600                 605
Val Phe Ile Asn Pro Ala Leu Val Glu Pro Phe Gly Leu Thr Ile Ile
    610                 615                 620
Glu Ala Ala Ala Tyr Gly Leu Pro Val Val Ala Thr Lys Asn Gly Gly
625                 630                 635                 640
Pro Val Asp Ile Leu Lys Ala Leu His Asn Gly Leu Leu Val Asp Pro
                645                 650                 655
His Ser Ala Glu Ala Ile Thr Gly Ala Leu Leu Ser Leu Leu Ala Glu
            660                 665                 670
Lys Ser Arg Trp Val Glu Cys Arg Arg Asn Gly Leu Arg Asn Ile His
        675                 680                 685
```

Arg Phe Ser Trp Pro His His Cys Arg Leu Tyr Leu Ser His Val Ser
690 695 700
Thr Tyr Cys Asp Gln Pro Ser Pro His Gln Pro Leu Arg Val Pro Leu
705 710 715 720
Ala Leu Gly Ser Ser Thr Ser Phe Gly Ala Asp Asp Ser Leu Ser Asp
725 730 735
Ser Leu Arg Gly Leu Ser Leu Gln Ile Ser Val Asp Ala Ser Ser Asp
740 745 750
Leu Asn Ala Ala Asp Ser Ala Ala Ala Ile Met Asp Ala Leu Arg Arg
755 760 765
Arg Pro Ala Ser Glu Lys Pro Ala Ser Ser Gly Ala Arg Ala Leu Gly
770 775 780
Phe Ala Pro Gly Arg Arg Glu Ser Leu Leu Val Val Ala Val Asp Cys
785 790 795 800
Tyr Gly Asp Asp Gly Lys Pro Asp Val Glu Gln Leu Lys Lys Ala Ile
805 810 815
Asp Ala Ala Val Ser Val Gly Glu Cys Ala Gly Ala Lys Gln Gly Tyr
820 825 830
Val Leu Ser Thr Gly Met Thr Ile Pro Glu Ala Ala Glu Ala Ile Lys
835 840 845
Ala Cys Gly Ala Asp Val Ala Ser Phe Asp Ala Leu Ile Cys Ser Ser
850 855 860
Gly Ala Glu Leu Cys Tyr Pro Trp Lys Glu Leu Val Ala Asp Glu Glu
865 870 875 880
Tyr Ser Gly His Val Ala Phe Arg Trp Pro Gly Asp His Val Lys Ser
885 890 895
Ala Val Pro Arg Leu Gly Ser Met Glu Glu Ile Ala Leu Ala Ile Asp
900 905 910
Arg Pro Ala Ser Ser Val His Cys His Ala Tyr Ala Ala Thr Asp Ala
915 920 925
Ser Lys Val Ser Ile Thr Glu His Tyr Leu
930 935

<210> 169
<211> 808
<212> PRT
<213> Lolium perenne

<400> 169
Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu Arg Leu Gly
1 5 10 15
Ala Thr Phe Ser Ser His Pro Asn Glu Leu Ile Ala Leu Phe Ser Lys
20 25 30
Tyr Val His Gln Gly Lys Gly Met Leu Gln Arg His Gln Leu Leu Thr
35 40 45
Glu Phe Glu Ala Leu Phe Glu Ala Asp Lys Glu Arg Tyr Ala Pro Phe
50 55 60
Glu Asp Ile Leu Arg Ala Ala Gln Glu Ala Ile Val Leu Pro Pro Trp
65 70 75 80
Val Ala Leu Ala Ile Arg Pro Arg Pro Gly Val Trp Asp Tyr Ile Arg
85 90 95
Val Asn Val Ser Glu Leu Ala Val Glu Glu Leu Thr Val Ser Glu Tyr
100 105 110
Leu Ala Phe Lys Glu Gln Leu Val Asp Glu His Ala Ser Ser Lys Phe
115 120 125
Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ala Ser Phe Pro Arg Pro
130 135 140
Ser Met Ser Lys Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His
145 150 155 160
Leu Ser Ser Lys Leu Phe Gln Asp Lys Glu Ser Leu Tyr Pro Leu Leu
165 170 175
Asn Phe Leu Lys Ala His Asn His Lys Gly Thr Thr Met Met Leu Asn
180 185 190
Asp Arg Ile Gln Ser Leu Arg Gly Leu Gln Ser Ala Leu Arg Lys Ala
195 200 205

```
Glu Glu Tyr Leu Thr Ser Ile Pro Glu Asp Thr Pro Ser Ser Glu Phe
    210                 215                 220
Asn His Arg Phe Gln Glu Leu Gly Leu Glu Lys Gly Trp Gly Asp Thr
225                 230                 235                 240
Ala Lys Arg Val Gln Asp Thr Ile His Leu Leu Leu Asp Leu Leu Glu
                245                 250                 255
Ala Pro Asp Pro Ala Ser Leu Glu Lys Phe Leu Gly Thr Ile Pro Met
            260                 265                 270
Met Phe Asn Val Val Ile Leu Ser Pro His Gly Tyr Phe Ala Gln Ser
        275                 280                 285
Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val Tyr Ile Leu
    290                 295                 300
Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg Ile Lys Gln
305                 310                 315                 320
Gln Gly Leu Asp Ile Thr Pro Lys Ile Leu Ile Val Thr Arg Leu Leu
                325                 330                 335
Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu Lys Val Ile
            340                 345                 350
Gly Thr Glu His Thr Asp Ile Leu Arg Val Pro Phe Arg Thr Glu Lys
        355                 360                 365
Gly Ile Leu Arg Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu
    370                 375                 380
Glu Thr Tyr Thr Glu Asp Val Ala Asn Glu Leu Met Arg Glu Met Gln
385                 390                 395                 400
Thr Lys Pro Asp Leu Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val
                405                 410                 415
Ala Thr Leu Leu Ala His Lys Leu Gly Val Thr Gln Cys Thr Ile Ala
            420                 425                 430
His Ala Leu Glu Lys Thr Lys Tyr Pro Asn Ser Asp Ile Tyr Leu Asp
        435                 440                 445
Lys Phe Asp Ser Gln Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Leu
    450                 455                 460
Ile Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser Thr Phe Gln Glu
465                 470                 475                 480
Ile Ala Gly Ser Lys Asp Ser Val Gly Gln Tyr Glu Ser His Ile Ala
                485                 490                 495
Phe Thr Leu Pro Asp Leu Tyr Arg Val Val His Gly Ile Asp Val Phe
            500                 505                 510
Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp Met Thr Val Tyr
        515                 520                 525
Phe Pro Tyr Thr Glu Thr Asp Lys Arg Leu Thr Ala Phe His Pro Glu
    530                 535                 540
Ile Glu Glu Leu Leu Tyr Ser Asp Val Glu Asn Ser Glu His Lys Phe
545                 550                 555                 560
Val Leu Lys Asp Lys Asn Lys Pro Ile Ile Phe Ser Met Ala Arg Leu
                565                 570                 575
Asp Arg Val Lys Asn Met Thr Gly Leu Val Glu Met Phe Gly Lys Asn
            580                 585                 590
Ala His Leu Lys Asp Leu Ala Asn Leu Val Ile Val Ala Gly Asp His
        595                 600                 605
Gly Lys Glu Ser Lys Asp Arg Glu Glu Gln Ala Glu Phe Lys Arg Met
    610                 615                 620
Tyr Ser Leu Ile Glu Glu Tyr Lys Leu Glu Gly His Ile Arg Trp Ile
625                 630                 635                 640
Ser Ala Gln Met Asn Arg Val Arg Asn Ala Glu Leu Tyr Arg Tyr Ile
                645                 650                 655
Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Phe Tyr Glu Ala Phe
            660                 665                 670
Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Ile Ala
        675                 680                 685
Thr Cys His Gly Gly Pro Ala Glu Ile Ile Val Asn Gly Val Ser Gly
    690                 695                 700
Leu His Ile Asp Pro Tyr His Ser Asp Lys Ala Ala Asp Ile Leu Val
705                 710                 715                 720
Asn Phe Phe Glu Lys Ser Thr Ala Asp Pro Thr Tyr Trp Asp Lys Met
                725                 730                 735
```

Ser Glu Gly Gly Leu Lys Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Leu
740 745 750
Tyr Ser Glu Arg Leu Met Thr Leu Thr Gly Val Tyr Gly Phe Trp Lys
755 760 765
Tyr Val Ser Asn Leu Glu Arg Arg Glu Thr Arg Arg Tyr Leu Glu Met
770 775 780
Phe Tyr Ala Leu Lys Tyr Arg Ser Leu Ala Ala Ala Val Pro Leu Ala
785 790 795 800
Val Asp Gly Glu Asn Thr Asp Asn
805

<210> 170
<211> 815
<212> PRT
<213> Lolium perenne

<400> 170
Met Gly Glu Ala Ala Gly Asp Arg Val Leu Ser Arg Leu His Ser Val
1 5 10 15
Arg Glu Arg Ile Gly Asp Ser Leu Ser Ala His Pro Asn Glu Leu Val
20 25 30
Ala Val Phe Thr Arg Leu Val Asn Leu Gly Lys Gly Met Leu Gln Pro
35 40 45
His Gln Ile Ile Ala Glu Tyr Asn Thr Ala Ile Pro Glu Ala Glu Arg
50 55 60
Glu Lys Leu Lys Asp Gly Ala Phe Glu Asp Val Leu Arg Ala Ala Gln
65 70 75 80
Glu Ala Ile Val Ile Ser Pro Trp Val Ala Leu Ala Ile Arg Pro Arg
85 90 95
Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val Ser Glu Leu Ala Val
100 105 110
Glu Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Gln Leu Val
115 120 125
Glu Gly Ser Asn Lys Asp Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
130 135 140
Asn Ala Ser Phe Pro Arg Pro Ser Leu Ser Lys Ser Ile Gly Asn Gly
145 150 155 160
Val Gln Phe Leu Asn Arg His Leu Ser Ser Lys Leu Phe His Asp Lys
165 170 175
Glu Ser Met Tyr Pro Leu Leu Asn Phe Leu Arg Ala His Asn Tyr Lys
180 185 190
Gly Met Pro Met Met Met Asn Asp Arg Val Arg Ser Leu Ser Ala Leu
195 200 205
Gln Gly Ala Leu Arg Lys Ala Glu Glu His Leu Ser Gly Leu Pro Ala
210 215 220
Asp Thr Pro Tyr Ser Asp Phe His His Arg Phe Gln Glu Leu Gly Leu
225 230 235 240
Glu Lys Gly Trp Gly Asp Cys Ala Lys Arg Ala Gln Glu Thr Leu His
245 250 255
Leu Leu Leu Asp Leu Leu Glu Ala Pro Asp Pro Ser Thr Leu Glu Lys
260 265 270
Phe Leu Gly Thr Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
275 280 285
His Gly Tyr Phe Ala Gln Ala Asn Val Leu Gly Tyr Pro Asp Thr Gly
290 295 300
Gly Gln Val Val Tyr Ile Leu Asp Gln Val Arg Ala Met Glu Asn Glu
305 310 315 320
Met Leu Leu Arg Ile Lys Gln Gln Gly Leu Asp Ile Thr Pro Arg Ile
325 330 335
Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Thr Gly Thr Thr Cys Gly
340 345 350
Gln Arg Leu Glu Lys Val Leu Gly Thr Glu His Thr His Ile Leu Arg
355 360 365
Val Pro Phe Arg Thr Glu Asn Gly Ile Val Arg Lys Trp Ile Ser Arg
370 375 380
Phe Glu Val Trp Pro Tyr Leu Glu Thr Phe Thr Asp Asp Val Ala His

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385                 390                 395                 400
Glu Ile Ser Gly Glu Leu Gln Ala Asn Pro Asp Leu Ile Ile Gly Asn
                405                 410                 415
Tyr Ser Asp Gly Asn Leu Val Ala Cys Leu Leu Ala His Lys Met Gly
            420                 425                 430
Val Thr His Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
        435                 440                 445
Asn Ser Asp Leu Tyr Trp Lys Lys Phe Glu Asp His Tyr His Phe Ser
    450                 455                 460
Cys Gln Phe Thr Thr Asp Leu Ile Ala Met Asn His Ala Asp Phe Ile
465                 470                 475                 480
Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Asn Lys Asp Thr Val Gly
                485                 490                 495
Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Met Tyr Arg Val
            500                 505                 510
Val His Gly Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro
        515                 520                 525
Gly Ala Asp Met Ser Ile Tyr Phe Pro Tyr Ser Glu Ser Gln Arg Arg
    530                 535                 540
Leu Thr Ser Leu His Pro Glu Ile Glu Glu Leu Leu Tyr Ser Asp Val
545                 550                 555                 560
Asp Asn Asp Glu His Lys Phe Val Leu Lys Asp Arg Asn Lys Pro Ile
                565                 570                 575
Ile Phe Ser Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu
            580                 585                 590
Val Glu Leu Tyr Gly Arg Asn Pro Arg Leu Gln Glu Leu Val Asn Leu
        595                 600                 605
Val Val Val Cys Gly Asp His Gly Asn Pro Ser Lys Asp Lys Glu Glu
    610                 615                 620
Gln Ala Glu Phe Lys Lys Met Phe Asp Leu Ile Glu Gln Tyr Asn Leu
625                 630                 635                 640
Asn Gly His Ile Arg Trp Ile Ser Ala Gln Met Asn Arg Val Arg Asn
                645                 650                 655
Ala Glu Leu Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln
            660                 665                 670
Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Ile Glu Ala Met Thr
        675                 680                 685
Cys Gly Leu Pro Thr Phe Ala Thr Ala Tyr Gly Gly Pro Ala Glu Ile
    690                 695                 700
Ile Val Asn Gly Val Ser Gly Tyr His Ile Asp Pro Tyr Gln Gly Asp
705                 710                 715                 720
Lys Ala Ser Ala Leu Leu Val Glu Phe Phe Glu Lys Cys Gln Gly Asp
                725                 730                 735
His Ser His Trp Thr Lys Ile Ser Leu Gly Gly Leu Gln Arg Ile Glu
            740                 745                 750
Glu Lys Tyr Thr Trp Lys Leu Tyr Ser Glu Arg Leu Met Thr Leu Thr
        755                 760                 765
Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser Asn Leu Glu Arg Arg Glu
    770                 775                 780
Thr Arg Arg Tyr Leu Glu Met Leu Tyr Ala Leu Lys Tyr Arg Thr Met
785                 790                 795                 800
Ala Ser Thr Val Pro Leu Ala Val Glu Gly Glu Pro Ser Ser Lys
                805                 810                 815
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<210> 171
<211> 581
<212> PRT
<213> Festuca arundinacea

<400> 171

```
Met Ala Gln Ala Trp Ala Phe Phe Leu Leu Ala Leu Phe Ser Phe Ser
1               5                   10                  15
Ser Tyr Val Ser Arg Ile Phe Leu Cys Ser Arg Asn Gly Glu Gly Ser
            20                  25                  30
Phe Leu Cys Ala Arg Ala Pro Glu Val Pro Ser Ile Ala Ser Asp Arg
        35                  40                  45
```

```
Tyr Arg Thr Ala Tyr His Phe Gln Pro His Lys Asn Trp Met Asn Asp
    50                  55                  60
Pro Asn Gly Pro Met Tyr Tyr Asn Gly Ile Tyr His Leu Phe Phe Gln
65                  70                  75                  80
His Asn Pro Asn Gly Pro Gln Trp Gly Asp Ile Val Trp Gly His Ser
                85                  90                  95
Val Ser Thr Asp Leu Val Asn Trp Ile Ile Leu Glu Pro Ala Ile Glu
            100                 105                 110
Pro Asp Thr Pro Gly Asp Ile Lys Gly Cys Trp Ser Gly Ser Ala Thr
        115                 120                 125
Val Ile Ser Gly Ser Gln Pro Val Ile Met Tyr Thr Gly Gly Asp Val
    130                 135                 140
Glu Asn His Gln Val Gln Asn Ile Ala Leu Pro Lys Asn Arg Ser Asp
145                 150                 155                 160
Pro Tyr Leu Ile Glu Trp Thr Lys Ala Cys Asn Asn Pro Val Leu Gln
                165                 170                 175
Pro Val Gly Pro Gly Met Asn Pro Gly Glu Phe Arg Asp Pro Thr Thr
            180                 185                 190
Gly Trp Ile Gly Pro Asp Gly Leu Trp Arg Ile Ser Ile Gly Ala Glu
        195                 200                 205
Val Asn Gly Tyr Ser Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu
    210                 215                 220
Asn Trp Ser Arg Val Asp His Pro Leu Tyr Ser Ser Ser Ala Ser Thr
225                 230                 235                 240
Met Trp Glu Cys Leu Asp Phe Phe Ala Val Leu Pro Gly Ser Asn Gly
                245                 250                 255
Gly Leu Asp Leu Ser Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu
            260                 265                 270
Lys Val Ser Val Asp Gln Cys Asp Lys Tyr Met Ile Gly Val Tyr Asp
        275                 280                 285
Leu Glu His Asp Ala Phe Val Pro Asp Thr Ile Leu Asp Asp Arg Trp
    290                 295                 300
Leu Leu Pro Arg Ile Asp Tyr Gly Asn Tyr Tyr Ala Ser Lys Ser Phe
305                 310                 315                 320
Phe Asp Ser Lys Asn Arg Arg Arg Ile Ile Trp Gly Trp Thr Asn Glu
                325                 330                 335
Ser Asp Ser Ser Ser Asp Asp Val Ala Lys Gly Trp Ala Gly Ile Tyr
            340                 345                 350
Ala Ile Pro Arg Thr Ile Trp Leu Asp Arg Asp Gly Lys Gln Leu Leu
        355                 360                 365
Gln Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Arg Asn Glu Ile Asn
    370                 375                 380
Tyr Gln Gly Leu Asp Leu Glu Lys Gly Asp Leu Tyr Glu Ile Lys Gly
385                 390                 395                 400
Val Asp Thr Leu Gln Ala Asp Val Glu Ile Asp Phe Glu Leu Thr Ser
                405                 410                 415
Ile Asp Asp Ala Asp Ser Phe Asp Pro Ser Trp Leu Leu Asp Pro Glu
            420                 425                 430
Lys His Cys Arg Glu Ala Gly Ala Ser Val His Gly Gly Ile Gly Pro
        435                 440                 445
Phe Gly Leu Val Ile Leu Ala Thr Gly Asp Met Glu Glu His Thr Val
    450                 455                 460
Val His Phe Arg Val Tyr Lys Ser Gln Lys Glu Tyr Met Ile Leu Met
465                 470                 475                 480
Cys Ser Asp Ile Arg Arg Ser Ser Leu Arg Gln Gly Leu Tyr Ala Pro
                485                 490                 495
Ala Tyr Gly Gly Phe Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile
            500                 505                 510
Ser Leu Arg Thr Leu Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly
        515                 520                 525
Gly Gly Arg Val Cys Ile Ile Ala Arg Val Tyr Pro Val Ala Ile Val
    530                 535                 540
Asp Asp Gly Ser Ala His Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr
545                 550                 555                 560
```

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Val Arg Val Pro Gln Ile Arg Ala Trp Ser Met Met Thr Ala Gln Val
                565                 570                 575
Asn Leu Lys Lys Gly
            580

<210> 172
<211> 562
<212> PRT
<213> Lolium perenne

<400> 172
Met Asn Gly Ile Glu His Pro Gly Asn Gly Arg Thr Ala Tyr His Phe
 1               5                  10                  15
Gln Pro Ala Lys His Trp Gln Asn Asp Pro Asn Gly Pro Met Tyr His
            20                  25                  30
Asn Gly Leu Tyr His Phe Phe Tyr Gln Tyr Asn Pro His Gly Pro Thr
        35                  40                  45
Trp Asp Thr Gly Lys Leu Ser Trp Gly His Ser Val Ser Gly Asp Leu
    50                  55                  60
Val Asn Trp Ala Ala Leu Asp Asn Ala Leu Asp Pro Thr Ala Pro Phe
65                  70                  75                  80
Asp Ala Asn Gly Cys Trp Ser Gly Ser Ala Thr Ile Leu Pro Gly Gly
                85                  90                  95
Arg Pro Ala Ile Leu Tyr Thr Gly Ile Asp Ala Asp Lys Val Gln Val
            100                 105                 110
Gln Asn Val Ala Phe Ala Lys Asp Pro Ser Asp Pro Leu Leu Arg Glu
        115                 120                 125
Trp Glu Lys Pro Ser Cys Asn Pro Val Ile Pro Tyr Pro Ala Asp Val
    130                 135                 140
Thr Gly Asn Asn Phe Arg Asp Pro Thr Glu Ala Trp Arg Gly Arg Asp
145                 150                 155                 160
Gly Leu Trp Arg Val Gly Ile Val Ala Glu Val Lys Gly Val Gly Ser
                165                 170                 175
Leu Leu Val Tyr Arg Ser Ala Asp Phe Leu Arg Trp Gln Arg Asn Ala
            180                 185                 190
Ala Pro Leu His Ala Ser Ser Arg Asp Val Pro Val Leu Glu Cys Pro
        195                 200                 205
Asp Leu Phe Pro Val Ala Ala Ala Ala Gln Gly Ala Thr Glu Gly Leu
    210                 215                 220
Glu Thr Ser Ala Pro Ser Gly Ala Gly Val Arg His Val Leu Lys Leu
225                 230                 235                 240
Thr Asp Phe Ala Lys Glu Asp His Tyr Met Val Gly Phe Tyr Asp Asp
                245                 250                 255
Val Ala Asp Thr Phe Val Pro Ala Glu Pro Glu Arg Gly Asp Asp Pro
            260                 265                 270
Asp Asn Trp Arg Arg Leu Asp His Gly His Leu Tyr Ala Ser Lys Ser
        275                 280                 285
Phe Tyr Asp Ala Arg Asn Lys Arg Arg Ile Leu Trp Ala Trp Val Asp
    290                 295                 300
Glu Thr Asp Gly Gly Gly Val Ala Arg Gly Trp Ala Gly Ile Gln Ala
305                 310                 315                 320
Phe Pro Arg Ala Met Trp Leu Asp Ala Asp Gly Lys Arg Leu Val Gln
                325                 330                 335
Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg Lys Arg Val Gly Leu
            340                 345                 350
Arg Trp Ala Thr Asp Val Glu Ala Gly Gly Arg Lys Glu Ile Ala Gly
        355                 360                 365
Ile Val Ser Ser Gln Ala Asp Val Glu Val Val Phe Glu Ile Pro Asn
    370                 375                 380
Leu Glu Glu Ala Glu Thr Leu Asp Pro Glu Trp Val Leu Asp Pro Lys
385                 390                 395                 400
Gly Leu Cys Ala Ala Lys Gly Ala Ser Val His Gly Gly Val Gly Pro
                405                 410                 415
Phe Gly Leu Leu Val Leu Ala Ser Gly Asp Leu Glu Glu His Thr Ala
            420                 425                 430
Val Phe Phe Arg Val Phe Lys His Asp Gly Lys Tyr Lys Val Leu Met
```

```
        435                 440                 445
Cys Thr Asp Leu Thr Lys Ser Ser Thr Lys Ala Gly Ala His Lys Pro
    450                 455                 460
Ser Tyr Gly Ala Phe Leu Asp Val Asp Val Glu Lys Asp Lys Phe Ile
465                 470                 475                 480
Ser Leu Arg Thr Leu Ile Asp His Thr Val Val Glu Ser Phe Gly Asp
                485                 490                 495
Gly Gly Arg Thr Cys Met Thr Ala Arg Val Tyr Pro Glu His Ala Ala
            500                 505                 510
Met Gly Ser Thr His Leu Tyr Val Phe Asn Asn Gly Thr Gly Ala Val
        515                 520                 525
Lys Val Ser Lys Leu Glu Ala Trp Glu Leu Ala Thr Ala Ala Val Asn
    530                 535                 540
Gly Gly Ser Leu Ala Pro Val Val Val Lys Ala Ser Asp Pro Lys Glu
545                 550                 555                 560
Ala Leu


<210> 173
<211> 580
<212> PRT
<213> Festuca arundinacea

<400> 173
Met Ala His Ala Trp Ala Phe Phe Leu Leu Ala Leu Phe Ser Phe Ser
 1               5                  10                  15
Ser Cys Val Ser Lys Leu Phe Ile Tyr Ser Arg Asn Gly Glu Gly Ser
            20                  25                  30
Phe Leu Cys Thr Arg Ser Pro Glu Val Pro Ser Ile Ala Ser Lys Arg
        35                  40                  45
Tyr Arg Thr Ala Tyr His Phe Gln Ser Pro Lys Asn Trp Ile Asn Asp
    50                  55                  60
Pro Cys Gly Pro Met Tyr Tyr Asn Gly Ile Tyr His Glu Phe Tyr Gln
65                  70                  75                  80
Tyr Asn Pro Gly Gly Thr Ile Ala Ala Asn Ile Val Trp Gly His Ser
                85                  90                  95
Val Ser Thr Asp Leu Val Asn Trp Ile Gln Leu Glu Pro Ala Ile Val
            100                 105                 110
Arg Asp Thr Pro Tyr Asp Ile His Gly Cys Trp Thr Gly Ser Ile Thr
        115                 120                 125
Ile Leu Pro Gly Asp Gln Pro Val Ile Ile Tyr Thr Gly Arg Asp Ser
    130                 135                 140
Asp Asn His Gln Ser Gln Asn Ile Glu Leu Pro Lys Asn Arg Ser Asp
145                 150                 155                 160
Pro Tyr Leu Arg Glu Trp Thr Lys Ala Asp Asn Asn Pro Arg Ile Leu
                165                 170                 175
Pro Val Gly Pro Asp Leu Asn Leu Thr Gln Phe Arg Asp Pro Thr Thr
            180                 185                 190
Gly Trp Ile Gly Pro Asp Gly Leu Trp Arg Ile Ala Ile Gly Ala Glu
        195                 200                 205
Leu Asn Gly Tyr Gly Ala Ala Leu Leu Tyr Lys Ser Glu Asp Phe Leu
    210                 215                 220
Asn Trp Thr Arg Val Asp His Pro Leu Tyr Ser Asp Asn Ala Pro Ser
225                 230                 235                 240
Met Trp Glu Cys Pro Asp Phe Phe Ala Val Leu Pro Gly Asn Asn Gly
                245                 250                 255
Gly Leu Asp Leu Ser Ala Ala Ile Pro Lys Gly Ala Lys His Val Leu
            260                 265                 270
Lys Met Ser Val Asp Tyr Ser Asp Lys Tyr Met Ile Gly Val Tyr Asp
        275                 280                 285
Leu Lys Arg Asp Ala Phe Val Pro Asp Val Val Leu Asp Asp Arg Arg
    290                 295                 300
Leu Trp Leu Arg Ile Asp Tyr Gly Thr Phe Tyr Ala Ser Lys Ser Phe
305                 310                 315                 320
Phe Asp Ser Lys Arg Gly Arg Arg Val Ile Trp Gly Trp Ser Asn Glu
                325                 330                 335
```

Thr Asp Ser Val Ser Asp Asp Gly Ala Lys Gly Trp Ala Gly Ile His
            340   345   350
Ala Ile Pro Arg Ser Ile Trp Leu Asp Ser Asp Gly Lys Gln Leu Leu
        355   360   365
Gln Trp Pro Ile Asp Glu Ile Glu Ser Leu Arg Arg Asp Glu Ile Asn
    370   375   380
His Gln Gly Leu Glu Leu Lys Asn Gly Asp Leu Phe Glu Ile Lys Gly
385   390   395   400
Ile Asp Thr Leu Gln Ala Asp Ile Glu Val Asp Phe Glu Leu Thr Ser
                405   410   415
Ile Asp Ser Ala Asp Pro Phe Asp Pro Ser Trp Leu Leu Asp Val Glu
            420   425   430
Arg His Cys Arg Glu Ala Gly Ala Ser Val Gln Gly Gly Ile Gly Pro
        435   440   445
Phe Gly Leu Val Val Leu Ala Ser Asp Asn Met Glu Glu His Ile Ala
    450   455   460
Val His Phe Arg Val Tyr Lys Ser Gln Lys Ser His Met Ile Leu Met
465   470   475   480
Cys Ser Asp Leu Arg Arg Ser Ser Leu Arg Ser Gly Leu Tyr Thr Pro
                485   490   495
Ala Tyr Gly Gly Phe Phe Glu Phe Asp Leu Glu Lys Glu Arg Lys Ile
            500   505   510
Ser Leu Arg Thr Leu Ile Asp Arg Ser Ala Val Glu Ser Phe Gly Gly
        515   520   525
Gly Gly Arg Val Cys Ile Thr Ala Arg Ile Tyr Pro Val Ala Leu Val
    530   535   540
Asp Gly Arg Val His Met Tyr Ala Phe Asn Asn Gly Ser Thr Thr Val
545   550   555   560
Arg Val Pro Gln Leu Gly Ala Trp Ser Met Met Thr Ala Gln Val Asn
                565   570   575
Val Asn Lys Gly
            580

<210> 174
<211> 569
<212> PRT
<213> Festuca arundinacea Lolium perenne

<400> 174
Met Ala Gln Gly Trp Pro Phe Phe Leu Leu Val Leu Phe Ser Ser Cys
1   5   10   15
Val Ser Asn His Leu Val Asn Gly Glu Arg Val Phe Leu Phe Pro Gln
            20   25   30
Ser His Lys Val Ser Ser Ile Val Ser Lys Arg Tyr Arg Thr Ala Tyr
        35   40   45
His Phe Gln Pro Pro Lys Asn Trp Ile Asn Gly Pro Met Tyr Tyr Asn
    50   55   60
Gly Ile Tyr His Glu Phe Tyr Gln Tyr Asn Pro Asn Gly Ser Leu Trp
65   70   75   80
Gly Asn Ile Ile Trp Gly His Ser Val Ser Thr Asp Leu Ile Asn Trp
                85   90   95
Ile Pro Val Glu Pro Ala Ile Glu Arg Asp Ile Pro Ser Asp Ile Asn
            100   105   110
Gly Cys Trp Thr Gly Ser Ala Thr Ile Ile Ser Gly Asp Gln Pro Ile
        115   120   125
Ile Ile Tyr Thr Gly Ala Asp Lys Glu Asn Arg Gln Leu Gln Asn Ile
    130   135   140
Val Leu Pro Lys Asn Lys Ser Asp Pro Tyr Leu Arg Glu Trp Thr Lys
145   150   155   160
Ala Gly Asn Asn Pro Val Ile Gln Pro Val Gly Pro Gly Leu Asn Ala
                165   170   175
Ser Gln Phe Arg Asp Pro Thr Thr Gly Trp Ile Gly Pro Asp Gly Leu
            180   185   190
Trp Arg Ile Ala Val Gly Ala Glu Leu Asn Gly Tyr Gly Ala Ala Leu
        195   200   205
Leu Tyr Lys Ser Gln Asp Phe Leu Asn Trp Thr Arg Val Asp His Pro

```
    210                 215                 220
Leu Tyr Ser Ser Asn Ala Ser Ser Met Trp Glu Cys Pro Asp Phe Phe
225                 230                 235                 240
Ala Val Leu Pro Gly Asn Ser Gly Gly Leu Asp Leu Ser Ala Glu Ile
                245                 250                 255
Pro Asn Gly Ala Lys His Val Leu Lys Met Ser Leu Asp Ser Cys Asp
            260                 265                 270
Lys Tyr Met Ile Gly Val Tyr Asp Leu Lys Ser Asp Thr Phe Met Pro
        275                 280                 285
Asp Ser Val Leu Asp Asp Arg Arg Leu Trp Ser Arg Ile Asp His Gly
    290                 295                 300
Asn Phe Tyr Ala Ser Lys Ser Phe Phe Asp Ser Lys Lys Gly Arg Arg
305                 310                 315                 320
Ile Ile Trp Gly Trp Thr Asn Glu Thr Asp Ser Ser Ser Asp Asp Val
                325                 330                 335
Ala Lys Gly Trp Ala Gly Ile His Ala Ile Pro Arg Thr Ile Trp Leu
            340                 345                 350
Asp Ser Tyr Gly Lys Gln Leu Leu Gln Trp Pro Ile Glu Glu Ile Glu
        355                 360                 365
Ser Leu Arg Arg Asn Glu Ile Ser His Gln Gly Leu Glu Leu Lys Lys
    370                 375                 380
Gly Asp Leu Phe Glu Ile Lys Gly Thr Asp Thr Ser Gln Ala Asp Val
385                 390                 395                 400
Glu Val Asp Phe Glu Leu Thr Ser Ile Asp Asn Ala Asp Pro Phe Asp
                405                 410                 415
Pro Ser Trp Leu Leu Asp Val Glu Lys Gln Cys Arg Glu Ala Gly Ala
            420                 425                 430
Ser Val Gln Gly Gly Ile Gly Pro Phe Gly Leu Val Val Leu Ala Ser
        435                 440                 445
Asp Asn Met Glu Glu His Thr Ala Val His Phe Arg Val Tyr Lys Ser
    450                 455                 460
Gln Gln Ser Tyr Met Ile Leu Met Cys Ser Asp Leu Arg Arg Ser Ser
465                 470                 475                 480
Leu Arg Ser Gly Met Tyr Thr Pro Ala Tyr Gly Gly Phe Phe Glu Phe
                485                 490                 495
Asp Leu Gln Lys Glu Arg Lys Ile Ser Leu Arg Thr Leu Ile Asp Arg
            500                 505                 510
Ser Ala Val Glu Ser Phe Gly Gly Gly Gly Arg Val Cys Ile Met Ala
        515                 520                 525
Arg Val Tyr Pro Val Val Leu Val Asp Asp Gly Gly Ala His Met Tyr
    530                 535                 540
Ala Phe Asn Asn Gly Ser Thr Thr Val Arg Val Pro Gln Leu Arg Ala
545                 550                 555                 560
Trp Ser Met Ser Arg Ala Glu His Lys
                565

<210> 175
<211> 588
<212> PRT
<213> Lolium perenne

<400> 175
Met Gly Val Arg Leu Gly Arg Val Ala Trp Ala Cys Pro Ala Val Leu
1               5                   10                  15
Val Leu Leu Leu Gln Leu Ala Gly Ala Ser His Val Val Tyr Glu Thr
            20                  25                  30
Ser Leu Leu Glu Thr Glu Ala Ala Ala Ala Thr Val Pro Ala Ser Ile
        35                  40                  45
Phe Glu Leu Ser Thr Gly Tyr His Phe Arg Pro Gln Lys Asn Trp Ile
    50                  55                  60
Asn Asp Pro Asn Ala Pro Leu Tyr Tyr Lys Gly Trp Tyr His Leu Phe
65                  70                  75                  80
Phe Gln Tyr Asn Pro Lys Gly Ala Val Trp Gly Asn Ile Val Trp Ala
                85                  90                  95
His Ser Val Ser Arg Asp Leu Ile Asn Trp Val Ala Leu Glu Thr Ala
            100                 105                 110
```

Leu Ala Pro Ser Ile Asp Ala Asp Lys Tyr Gly Cys Trp Ser Gly Ser
115 120 125
Ala Thr Ile Met Pro Asp Gly Thr Pro Val Ile Met Tyr Thr Gly Val
130 135 140
Ser Arg Pro Asp Val Asn Tyr Glu Val Gln Asn Val Ala Phe Pro Lys
145 150 155 160
Asn Ser Ser Asp Pro Leu Leu Arg Glu Trp Val Lys Pro Ala His Asn
165 170 175
Pro Val Ile Val Pro Glu Gly Gly Ile Asn Ala Thr Gln Phe Arg Asp
180 185 190
Pro Thr Thr Ala Trp Tyr Ala Asp Gly His Trp Arg Ile Leu Val Gly
195 200 205
Ala Leu Ser Gly Ala Ser Arg Gly Val Ala Tyr Val Tyr Arg Ser Arg
210 215 220
Asp Phe Arg Arg Trp Thr Arg Val Arg Lys Pro Leu His Ser Ala Pro
225 230 235 240
Thr Gly Met Trp Glu Cys Pro Asp Phe Tyr Pro Val Thr Val Asp Gly
245 250 255
Lys Glu Ser Gly Val Asp Thr Ser Val Val Ser Ser Ser Arg Val Lys
260 265 270
His Val Leu Lys Asn Ser Leu Asp Leu Arg Arg Tyr Asp Tyr Tyr Thr
275 280 285
Val Gly Thr Tyr Asp Arg Leu Lys Glu Arg Tyr Val Pro Asp Asn Pro
290 295 300
Ala Gly Asp Lys His His Leu Arg Tyr Asp Tyr Gly Asn Phe Tyr Ala
305 310 315 320
Ser Lys Thr Phe Tyr Asp Pro Ser Lys Arg Arg Arg Ile Leu Trp Gly
325 330 335
Trp Ala Asn Glu Ser Asp Thr Ala Val Asp Asp Val Ala Lys Gly Trp
340 345 350
Ala Gly Ile Gln Ala Ile Pro Arg Lys Val Trp Leu Asp Pro Ser Gly
355 360 365
Arg Gln Leu Met Gln Trp Pro Val Glu Glu Val Glu Ala Leu Arg Gly
370 375 380
Lys Lys Pro Val Ser Leu Lys Asp Arg Met Val Lys Arg Gly Glu His
385 390 395 400
Val Glu Val Thr Gly Leu Gln Thr Ala Gln Ala Asp Val Glu Val Ser
405 410 415
Phe Glu Val Pro Ser Leu Glu Gly Ala Glu Ala Leu Asp Pro Ala Leu
420 425 430
Ala Asn Asp Ala Gln Lys Leu Cys Gly Val Lys Gly Ala Asp Val Glu
435 440 445
Gly Gly Val Gly Pro Phe Gly Leu Trp Val Leu Ala Ser Ser Lys Leu
450 455 460
Glu Glu Arg Thr Ala Val Phe Phe Arg Val Phe Lys Ala Ala Gly Asn
465 470 475 480
Val Asn Ser Thr Lys Pro Leu Val Leu Met Cys Ser Asp Pro Thr Lys
485 490 495
Ser Ser Leu Asn Lys Asn Leu Tyr His Pro Thr Phe Ala Gly Phe Val
500 505 510
Asp Ile Asp Met Ala Lys Gly Lys Ile Ser Leu Arg Ser Leu Ile Asp
515 520 525
Gln Ser Val Val Glu Ser Phe Gly Ala Gly Gly Arg Thr Cys Ile Leu
530 535 540
Ser Arg Val Tyr Pro Ser Leu Ala Ile Gly Arg Asn Ala His Leu His
545 550 555 560
Val Phe Asn Asn Gly Lys Ala Asp Ile Lys Val Ser Arg Leu Thr Ala
565 570 575
Trp Glu Met Lys Lys Pro Ala Leu Met Asn Gly Ala
580 585

<210> 176
<211> 670
<212> PRT
<213> Lolium perenne

<400> 176

Met Pro Met Glu Ala Arg Asp Gly Val Ser Met Pro Tyr Ser Tyr Ala
1 5 10 15
Ala Leu Pro Glu Asp Ala Glu Ala Ala Val Val Gly Arg Gly Arg Arg
20 25 30
Thr Gly Pro Leu Phe Ala Ala Leu Leu Leu Thr Leu Val Ala Ala Leu
35 40 45
Leu Ala Val Ala Ala Leu Ala Gly Val Arg Leu Val Gly Glu Leu Pro
50 55 60
Ala Gly Gly Val Val Met Pro Asn His Pro Met Glu Val Met Asp Val
65 70 75 80
Ser Gly Ser Arg Gly Pro Glu Ser Gly Val Ser Glu Lys Thr Ser Gly
85 90 95
Ala Ala Ser Glu Ser Gly Gly Met Leu Gly Ala Asp Ala Gly Ser Asn
100 105 110
Ala Phe Pro Trp Ser Asn Ala Met Leu Gln Trp Gln Arg Thr Gly Phe
115 120 125
His Phe Gln Pro Glu Lys Asn Trp Met Asn Asp Pro Asn Gly Pro Val
130 135 140
Tyr Tyr Lys Gly Trp Tyr His Leu Phe Tyr Gln Tyr Asn Pro Glu Gly
145 150 155 160
Ala Ile Trp Gly Asn Lys Ile Ala Trp Gly His Ala Val Ser Arg Asp
165 170 175
Met Leu Arg Trp Arg His Leu Pro Ile Ala Met Phe Pro Asp Gln Trp
180 185 190
Tyr Asp Ile Asn Gly Ala Trp Ser Gly Ser Ala Thr Val Leu Pro Asp
195 200 205
Gly Arg Ile Val Met Leu Tyr Thr Gly Ser Thr Asn Ala Ser Val Gln
210 215 220
Val Gln Cys Leu Ala Phe Pro Ser Asp Pro Ser Asp Pro Leu Leu Thr
225 230 235 240
Asn Trp Thr Lys Tyr Glu Gly Asn Pro Val Leu Tyr Pro Pro Pro His
245 250 255
Val Gly Glu Lys Asp Phe Arg Asp Pro Thr Thr Ala Trp Tyr Asp Gly
260 265 270
Ser Asp Gly Met Trp Arg Ile Val Ile Gly Ser Lys Asp Asn Arg Arg
275 280 285
Ala Gly Met Ala Leu Thr Tyr Lys Thr Lys Asn Phe His Asp Phe Glu
290 295 300
Leu Val Pro Gly Val Leu His Arg Val Pro Ala Thr Gly Met Trp Glu
305 310 315 320
Cys Ile Asp Leu Tyr Pro Val Gly Gly Ala Arg Gly Ile Asp Met Thr
325 330 335
Glu Ala Val Ala Ala Ala Ser Asn Ser Gly Gly Gly Glu Val Leu His
340 345 350
Val Met Lys Glu Ser Ser Asp Asp Asp Arg His Asp Tyr Tyr Ala Leu
355 360 365
Gly Arg Tyr Asp Ala Ala Thr Asn Lys Trp Thr Pro Leu Asp Ala Asp
370 375 380
Ala Asp Val Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala
385 390 395 400
Ser Lys Thr Phe Tyr Asp Pro Ala Lys Lys Arg Arg Val Leu Trp Gly
405 410 415
Trp Val Gly Glu Thr Asp Ser Glu Arg Ala Asp Val Ala Lys Gly Trp
420 425 430
Ala Ser Leu Gln Ser Ile Pro Arg Thr Val Val Leu Asp Thr Lys Thr
435 440 445
Gly Ser Asn Leu Ile Gln Trp Pro Val Val Glu Val Glu Thr Leu Arg
450 455 460
Thr Asn Ser Thr Asn Leu Gly Ser Ile Ile Val Glu His Gly Ser Val
465 470 475 480
Phe Pro Leu Ser Leu His Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser
485 490 495
Phe Arg Leu Asp Pro Leu Asp Val Ala Ala Ala Lys Glu Ala Asp Val
500 505 510
Gly Tyr Asn Cys Ser Thr Ser Gly Gly Ala Ala Gly Arg Gly Ala Leu

```
        515                 520                 525
Gly Pro Phe Gly Leu Leu Val Leu Ala Asp Ala Arg Arg His Gly Gly
    530                 535                 540
Asp Thr Glu Gln Thr Ala Val Tyr Phe Tyr Val Ala Arg Gly Leu Asp
545                 550                 555                 560
Gly Asn Leu Arg Thr His Phe Cys His Asp Glu Ser Arg Ser Ser Arg
                565                 570                 575
Ala Asn Asp Ile Val Lys Arg Val Val Gly Asn Ile Val Pro Val Leu
            580                 585                 590
Asp Gly Glu Ala Leu Ser Val Arg Val Leu Val Asp His Ser Ile Val
        595                 600                 605
Glu Ser Phe Ala Gln Gly Gly Arg Ser Val Val Thr Ser Arg Val Tyr
    610                 615                 620
Pro Thr Glu Ala Ile Tyr Ala Asn Ala Gly Val Tyr Leu Phe Asn Asn
625                 630                 635                 640
Ala Thr Gly Ala Arg Val Thr Ala Thr Ser Leu Val Val His Glu Met
                645                 650                 655
Asp Pro Ser Tyr Asn Gln Asn Gln Ala Glu Met Ala Ser Leu
            660                 665                 670
```

<210> 177
<211> 514
<212> PRT
<213> Lolium perenne

<400> 177

```
Met His Ala Asp Pro Asn Gly Pro Val Tyr Tyr Arg Gly Trp Tyr His
1               5                   10                  15
Leu Phe Tyr Gln Tyr Asn Pro Glu Gly Ala Val Trp Gly Asn Ile Ala
            20                  25                  30
Trp Gly His Ala Val Ser Arg Asp Leu Val His Trp Arg His Leu Pro
        35                  40                  45
Leu Ala Met Val Pro Asp Gln Trp Tyr Asp Ile Asn Gly Val Trp Thr
    50                  55                  60
Gly Ser Ala Thr Val Phe Pro Asp Gly Thr Leu Asn Met Leu Tyr Thr
65                  70                  75                  80
Gly Ser Thr Asn Ala Ser Val Gln Ala Gln Cys Leu Ala Val Pro Glu
                85                  90                  95
Asp Pro Asn Asp Ser Leu Leu Arg Asn Trp Thr Lys His Glu Ala Asn
            100                 105                 110
Pro Val Leu Leu Pro Pro Pro Gly Ile Gly Asp Lys Asp Phe Arg Asp
        115                 120                 125
Pro Thr Thr Ala Trp Phe Asp Glu Ser Asp Gln Thr Trp Arg Thr Val
    130                 135                 140
Ile Gly Ser Lys Asp Asn Asn Gly His Ala Gly Ile Ala Met Val Tyr
145                 150                 155                 160
Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Tyr Leu His
                165                 170                 175
Arg Val Asp Gly Thr Gly Met Trp Glu Cys Ile Asp Phe Tyr Pro Val
            180                 185                 190
Gly Gly Lys Asn Gly Ser Glu Glu Leu Tyr Val Ile Lys Glu Ser Ser
        195                 200                 205
Asp Asp Asp Arg His Asp Trp Tyr Thr Leu Gly Lys Tyr Asp Ala Ala
    210                 215                 220
Ala Asn Thr Phe Thr Ala Ala Asp Pro Glu Asn Asp Leu Gly Ile Gly
225                 230                 235                 240
Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Lys Thr Phe Tyr Asp
                245                 250                 255
Pro Ala Lys Lys Arg Arg Val Leu Trp Gly Trp Ile Gly Glu Thr Asp
            260                 265                 270
Ser Glu Arg Ala Asp Val Ala Lys Gly Trp Ala Ser Leu Met Ser Ile
        275                 280                 285
Pro Arg Thr Val Glu Leu Asp Glu Lys Thr Trp Thr Asn Leu Ile Gln
    290                 295                 300
Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Ile Lys Ser Thr Asp Leu
305                 310                 315                 320
```

Gly Gly Ile Thr Ile Asp His Gly Ser Val Tyr Pro Leu Pro Leu His
325 330 335
Arg Ala Thr Gln Leu Asp Ile Glu Ala Ser Phe Arg Leu Asp Ala Ala
340 345 350
Thr Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Thr
355 360 365
Ser Gly Gly Ser Thr His Arg Gly Ala Leu Gly Pro Phe Gly Ile Leu
370 375 380
Val Leu Ala Asp Gly Lys Ala Glu Gln Thr Ala Val Tyr Phe Tyr Val
385 390 395 400
Ser Lys Gly Leu Asp Gly Ala Leu Glu Thr His Phe Cys His Asp Glu
405 410 415
Ser Arg Ser Thr Leu Ala Lys Asp Val Val Lys Arg Val Val Gly Tyr
420 425 430
Thr Val Pro Val Leu Asp Gly Glu Ala Phe Ser Val Arg Val Leu Val
435 440 445
Asp His Ser Ile Val Glu Ser Phe Ala Met Gly Gly Arg Ser Thr Ala
450 455 460
Thr Ser Arg Val Tyr Pro Thr Glu Ser Ile Tyr Gly Ala Ala Gly Ala
465 470 475 480
Tyr Leu Phe Asn Asn Ala Thr Gly Gly Ser Val Thr Val Glu Lys Leu
485 490 495
Val Val His Glu Met Asp Ser Ser Tyr Asn Gln Ile Phe Met Ala Asp
500 505 510
Asp Leu

<210> 178
<211> 557
<212> PRT
<213> Lolium perenne

<400> 178
Met Gly Ser Val Pro Glu Glu Ser Val Val Ser Val Ala Ala Ala Glu
1 5 10 15
Thr Val Phe Arg Ser Lys Leu Pro Asp Ile Glu Ile Asn Asn Glu Gln
20 25 30
Thr Leu Gln Ser Tyr Cys Phe Glu Lys Met Ala Glu Val Ala Ser Arg
35 40 45
Pro Cys Ile Ile Asp Gly Gln Thr Gly Ala Ser Tyr Thr Tyr Thr Glu
50 55 60
Val Asp Ser Leu Thr Arg Arg Ala Ala Ala Gly Leu Arg Arg Met Gly
65 70 75 80
Val Gly Lys Gly Asp Val Val Met Asn Leu Leu Arg Asn Cys Pro Glu
85 90 95
Phe Ala Phe Ser Phe Leu Gly Ala Ala Arg Leu Gly Ala Ala Thr Thr
100 105 110
Thr Ala Asn Pro Phe Tyr Thr Pro His Glu Ile His Arg Gln Ala Glu
115 120 125
Ala Ala Gly Ala Lys Leu Ile Val Thr Glu Ala Cys Ala Val Glu Lys
130 135 140
Val Leu Glu Phe Ala Ala Gly Arg Gly Leu Pro Val Val Thr Val Asp
145 150 155 160
Gly Arg Arg Asp Gly Cys Val Asp Phe Ala Glu Leu Ile Ala Gly Glu
165 170 175
Glu Leu Pro Glu Ala Asp Glu Ala Gly Ile Leu Pro Asp Asp Val Val
180 185 190
Ala Leu Pro Tyr Ser Ser Gly Thr Thr Gly Leu Pro Lys Gly Val Met
195 200 205
Leu Thr His Arg Ser Leu Val Thr Ser Val Ala Gln Leu Val Asp Gly
210 215 220
Ser Asn Pro Asn Val Cys Phe Asn Lys Asp Asp Ala Leu Leu Cys Leu
225 230 235 240
Leu Pro Leu Phe His Ile Tyr Ser Leu His Thr Val Leu Leu Ala Gly
245 250 255
Leu Arg Val Gly Ala Ala Ile Val Ile Met Arg Lys Phe Asp Val Gly

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                260                 265                 270
Ala Leu Val Asp Leu Val Arg Ala His Arg Ile Thr Ile Ala Pro Phe
            275                 280                 285
Val Pro Pro Ile Val Val Glu Ile Ala Lys Ser Asp Arg Val Gly Ala
    290                 295                 300
Asp Asp Leu Ala Ser Ile Arg Met Val Leu Ser Gly Ala Ala Pro Met
305                 310                 315                 320
Gly Lys Asp Leu Gln Asp Ala Phe Met Ala Lys Ile Pro Asn Ala Val
                325                 330                 335
Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala Gly Pro Val Leu Ala Met
            340                 345                 350
Cys Leu Ala Phe Ala Lys Glu Pro Phe Lys Val Lys Ser Gly Ser Cys
        355                 360                 365
Gly Thr Val Val Arg Asn Ala Glu Leu Lys Val Val Asp Pro Asp Thr
    370                 375                 380
Gly Ala Ser Leu Gly Arg Asn Gln Pro Gly Glu Ile Cys Val Arg Gly
385                 390                 395                 400
Lys Gln Ile Met Ile Gly Tyr Leu Asn Asp Pro Glu Ser Thr Lys Asn
                405                 410                 415
Thr Ile Asp Lys Asp Gly Trp Leu His Thr Gly Asp Ile Gly Leu Val
            420                 425                 430
Asp Asp Asp Asp Glu Ile Phe Ile Val Asp Arg Leu Lys Glu Ile Ile
        435                 440                 445
Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala Glu Leu Glu Ala Leu Leu
    450                 455                 460
Leu Thr Asn Pro Glu Val Lys Asp Ala Ala Val Val Gly Val Lys Asp
465                 470                 475                 480
Asp Leu Cys Gly Glu Val Pro Val Ala Phe Ile Lys Arg Ile Glu Gly
                485                 490                 495
Ser Glu Ile Thr Glu Asn Glu Ile Lys Gln Phe Val Ser Lys Glu Val
            500                 505                 510
Val Phe Tyr Lys Arg Ile Asn Lys Val Tyr Phe Thr Asp Ser Ile Pro
        515                 520                 525
Lys Asn Pro Ser Gly Lys Ile Leu Arg Lys Asp Leu Arg Ala Arg Leu
    530                 535                 540
Ala Ala Gly Ile Pro Thr Glu Val Ala Ala Pro Arg Ser
545                 550                 555

<210> 179
<211> 501
<212> PRT
<213> Lolium perenne

<400> 179
Met Glu Val Leu Leu Leu Glu Lys Ala Leu Leu Gly Leu Phe Ala Ala
1               5                   10                  15
Ala Val Leu Ala Ile Ala Val Ala Lys Leu Ala Gly Lys Arg Phe Arg
            20                  25                  30
Leu Pro Pro Gly Pro Ser Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
        35                  40                  45
Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Gly Ile Ala Lys Arg
    50                  55                  60
Phe Gly Glu Val Phe Leu Leu Arg Met Gly Ile Arg Asn Leu Val Val
65                  70                  75                  80
Val Ser Ser Pro Glu Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
                85                  90                  95
Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
            100                 105                 110
Asn Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
        115                 120                 125
Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
    130                 135                 140
Gln Asn Arg Val Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
145                 150                 155                 160
Val Lys Ala Asp Pro Ala Ser Ala Thr Ala Gly Thr Val Ile Arg Arg
                165                 170                 175
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Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
            180                 185                 190
Arg Arg Phe Glu Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
        195                 200                 205
Met Asn Ala Glu Arg Ser Ile Leu Ser Gln Ser Phe Asp Tyr Asn Tyr
    210                 215                 220
Gly Asp Phe Ile Pro Ile Leu Arg Pro Phe Leu Arg Lys Tyr Leu Asn
225                 230                 235                 240
Arg Cys Thr Asn Leu Lys Thr Lys Arg Met Lys Leu Phe Glu Asp His
                245                 250                 255
Phe Val Ala Asp Arg Lys Lys Ala Leu Glu Gln Asn Gly Glu Ile Arg
            260                 265                 270
Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
        275                 280                 285
His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
    290                 295                 300
Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
305                 310                 315                 320
His Pro Asp Val Gln Ser Lys Leu Arg Asp Glu Met Thr Ala Val Leu
                325                 330                 335
Gly Ala Asp Val Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr
            340                 345                 350
Leu Gln Ser Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro
        355                 360                 365
Leu Leu Val Pro His Met Asn Leu Ser Asp Ala Lys Leu Ala Gly Tyr
    370                 375                 380
Asp Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala
385                 390                 395                 400
Asn Asp Pro Lys Arg Trp Val Arg Ala Asp Glu Phe Arg Pro Glu Arg
                405                 410                 415
Phe Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg
            420                 425                 430
Phe Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Val Leu
        435                 440                 445
Ala Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Asn Phe
    450                 455                 460
Gln Leu Leu Pro Pro Pro Gly Gln Asp Lys Ile Asp Thr Thr Glu Lys
465                 470                 475                 480
Pro Gly Gln Phe Ser Asn Gln Ile Leu Lys His Ala Thr Val Val Cys
                485                 490                 495
Lys Pro Leu Glu Ala
            500

<210> 180
<211> 361
<212> PRT
<213> Lolium perenne

<400> 180
Met Gly Ser Val Asp Ala Ser Glu Lys Thr Ile Thr Gly Trp Ala Ala
1               5                   10                  15
Arg Asp Ala Thr Gly His Leu Ser Pro Tyr Thr Tyr Asn Leu Arg Arg
            20                  25                  30
Thr Gly Ala Glu Asp Val Val Leu Lys Val Leu Tyr Cys Gly Ile Cys
        35                  40                  45
His Thr Asp Leu His Gln Thr Lys Asn His Leu Gly Ala Ser Lys Tyr
    50                  55                  60
Pro Met Val Pro Gly His Glu Val Val Gly Glu Val Val Glu Val Gly
65                  70                  75                  80
Pro Glu Val Ser Lys Tyr Ser Val Gly Asp Val Val Gly Val Gly Val
                85                  90                  95
Ile Val Gly Cys Cys Arg Asp Cys Arg Pro Cys Lys Ala Asn Val Glu
            100                 105                 110
Gln Tyr Cys Asn Lys Lys Ile Trp Ser Tyr Asn Asp Val Tyr Thr Asp
        115                 120                 125
Gly Lys Pro Thr Gln Gly Gly Phe Ala Ser Ser Met Val Val Asp Gln
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130 135 140
Lys Phe Val Val Lys Ile Pro Ala Gly Leu Ala Pro Glu Gln Ala Ala
145 150 155 160
Pro Leu Leu Cys Ala Gly Val Thr Val Tyr Ser Pro Leu Lys His Phe
165 170 175
Gly Leu Met Thr Pro Gly Leu Arg Gly Gly Ile Leu Gly Leu Gly Gly
180 185 190
Val Gly His Met Gly Val Lys Val Ala Lys Ser Met Gly His His Val
195 200 205
Thr Val Ile Ser Ser Ser Asp Lys Lys Arg Ala Glu Ala Met Asp Asp
210 215 220
Leu Gly Ala Asp Ala Tyr Leu Val Ser Ser Asp Glu Ala Gln Met Ala
225 230 235 240
Ala Ala Met Asp Ser Leu Asp Tyr Ile Ile Asp Thr Val Pro Val Lys
245 250 255
His Pro Leu Glu Pro Tyr Leu Ala Leu Leu Lys Met Asp Gly Lys Leu
260 265 270
Val Leu Met Gly Val Ile Gly Glu Pro Leu Ser Phe Val Ser Pro Met
275 280 285
Val Met Leu Gly Arg Lys Thr Ile Thr Gly Ser Phe Ile Gly Ser Ile
290 295 300
Glu Glu Thr Glu Glu Val Leu Arg Phe Cys Val Asp Lys Gly Leu Thr
305 310 315 320
Ser Gln Ile Glu Val Val Lys Met Asp Tyr Leu Asn Gln Ala Leu Glu
325 330 335
Arg Leu Glu Arg Asn Asp Val Arg Tyr Arg Phe Val Val Asp Val Ala
340 345 350
Gly Ser Asn Ile Asp Asp Thr Ala Ala
355 360

<210> 181
<211> 363
<212> PRT
<213> Lolium perenne

<400> 181
Met Thr Val Val Glu Val Leu Ala Ala Gly Asp Ala Ala Ala Ala Ala
1 5 10 15
Val Ala Arg Pro Ala Gly Asn Gly Gln Thr Val Cys Val Thr Gly Ala
20 25 30
Ala Gly Tyr Ile Ala Ser Trp Leu Val Lys Leu Leu Leu Glu Lys Gly
35 40 45
Tyr Thr Val Lys Gly Thr Val Arg Asn Pro Asp Asp Pro Lys Asn Ala
50 55 60
His Leu Arg Ala Leu Asp Gly Ala Ala Asp Arg Leu Val Leu Cys Lys
65 70 75 80
Ala Asp Leu Leu Asp Tyr Asp Ala Ile Arg Arg Ala Ile Asp Gly Cys
85 90 95
His Gly Val Phe His Thr Ala Ser Pro Val Thr Asp Asp Pro Glu Gln
100 105 110
Met Val Glu Pro Ala Val Arg Gly Thr Gln Tyr Val Ile Asp Ala Ala
115 120 125
Ala Glu Ala Gly Thr Val Arg Arg Met Val Leu Thr Ser Ser Ile Gly
130 135 140
Ala Val Thr Met Asp Pro Asn Arg Gly Pro Asp Val Val Val Asp Glu
145 150 155 160
Ser Cys Trp Ser Asp Leu Asp Phe Cys Lys Lys Thr Arg Asn Trp Tyr
165 170 175
Cys Tyr Gly Lys Ala Val Ala Glu Gln Ala Ala Ser Glu Leu Ala Arg
180 185 190
Gln Arg Gly Val Asp Leu Val Val Val Asn Pro Val Leu Val Ile Gly
195 200 205
Pro Leu Leu Gln Pro Thr Val Asn Ala Ser Ile Gly His Ile Leu Lys
210 215 220
Tyr Leu Asp Gly Ser Ala Ser Lys Phe Ala Asn Ala Val Gln Ala Tyr
225 230 235 240

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Val Asp Val Arg Asp Val Ala Asp Ala His Leu Arg Val Phe Glu Cys
                245                 250                 255
Ala Ala Ala Ser Gly Arg His Leu Cys Ala Glu Arg Val Leu His Arg
            260                 265                 270
Glu Asp Val Val Arg Ile Leu Ala Lys Leu Phe Pro Glu Tyr Pro Val
        275                 280                 285
Pro Thr Arg Cys Ser Asp Glu Ala Asn Pro Arg Lys Gln Pro Tyr Lys
    290                 295                 300
Met Ser Asn Gln Lys Leu Gln Asp Leu Gly Leu Glu Phe Arg Pro Val
305                 310                 315                 320
Ser Gln Ser Leu Tyr Glu Thr Val Lys Ser Leu Gln Glu Lys Gly His
                325                 330                 335
Leu Pro Val Leu Ser Glu Gln Ala Glu Ala Asp Lys Glu Thr Leu Ala
            340                 345                 350
Ala Glu Leu Gln Ala Gly Val Thr Ile Arg Ala
        355                 360

<210> 182
<211> 360
<212> PRT
<213> Festuca arundinacea

<400> 182
Met Gly Ser Thr Ala Ala Asp Met Ala Ala Ser Ala Asp Glu Glu Ala
 1               5                  10                  15
Cys Met Phe Ala Leu Gln Leu Ala Ser Ser Ser Ile Leu Pro Met Thr
            20                  25                  30
Leu Lys Asn Ala Ile Glu Leu Gly Leu Leu Glu Ile Leu Val Ala Ala
        35                  40                  45
Gly Gly Lys Ser Leu Thr Pro Thr Glu Val Ala Ala Lys Leu Pro Ser
    50                  55                  60
Ala Ala Asn Pro Glu Ala Pro Asp Met Val Asp Arg Met Leu Arg Leu
65                  70                  75                  80
Leu Ala Ser Tyr Asn Val Val Thr Cys Leu Val Glu Glu Gly Lys Asp
                85                  90                  95
Gly Arg Leu Ser Arg Ser Tyr Gly Ala Ala Pro Val Cys Lys Phe Leu
            100                 105                 110
Thr Pro Asn Glu Asp Gly Val Ser Met Ala Ala Leu Ala Leu Met Asn
        115                 120                 125
Gln Asp Lys Val Leu Met Glu Ser Trp Tyr Tyr Leu Lys Asp Ala Val
    130                 135                 140
Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
145                 150                 155                 160
Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Arg Val Phe Asn Glu Gly
                165                 170                 175
Met Lys Asn His Ser Ile Ile Ile Thr Lys Lys Leu Leu Glu Leu Tyr
            180                 185                 190
His Gly Phe Gln Gly Leu Gly Thr Leu Val Asp Val Gly Gly Gly Val
        195                 200                 205
Gly Ala Thr Val Ala Ala Ile Ala Ala His Tyr Pro Ala Ile Lys Gly
    210                 215                 220
Val Asn Phe Asp Leu Pro His Val Ile Ser Glu Ala Pro Gln Phe Pro
225                 230                 235                 240
Gly Val Thr His Val Gly Gly Asp Met Phe Lys Glu Val Pro Ser Gly
                245                 250                 255
Asp Ala Ile Leu Met Lys Trp Ile Leu His Asp Trp Ser Asp Gln His
            260                 265                 270
Cys Ala Thr Leu Leu Lys Asn Cys Tyr Asp Ala Leu Pro Ala His Gly
        275                 280                 285
Lys Val Val Leu Val Glu Cys Ile Leu Pro Val Asn Pro Glu Ala Lys
    290                 295                 300
Pro Ser Ser Gln Gly Val Phe His Val Asp Met Ile Met Leu Ala His
305                 310                 315                 320
Asn Pro Gly Gly Arg Glu Arg Tyr Glu Arg Glu Phe Glu Ala Leu Ala
                325                 330                 335
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Arg Gly Ala Gly Phe Thr Gly Val Lys Ser Thr Tyr Ile Tyr Ala Asn
340 345 350
Ala Trp Ala Ile Glu Phe Thr Lys
355 360

<210> 183
<211> 543
<212> PRT
<213> Lolium perenne

<400> 183
Met Val Gly Phe Ala Lys Ile Ala Met Glu Trp Ile Gln Asp Pro Leu
1 5 10 15
Ser Trp Leu Phe Ile Ala Ser Val Val Phe Val Val Leu Gln Arg Arg
20 25 30
Arg Arg Gly Asn Val Ala Pro Phe Pro Pro Gly Pro Lys Pro Leu Pro
35 40 45
Ile Val Gly Asn Met Ser Met Met Asp Gln Leu Thr His Arg Gly Leu
50 55 60
Ala Ala Leu Ala Lys Glu Tyr Gly Gly Leu Leu His Ile Arg Leu Gly
65 70 75 80
Lys Leu His Thr Phe Ala Val Ser Thr Pro Glu Tyr Ala Arg Glu Val
85 90 95
Leu Gln Val Gln Asp Gly Ala Phe Ser Asn Arg Pro Ala Thr Ile Ala
100 105 110
Ile Ala Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr
115 120 125
Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe
130 135 140
Ser Arg Arg Arg Pro Glu Thr Trp Leu Ala Val Arg Asp Glu Ser Ala
145 150 155 160
Ala Leu Val Arg Ala Val Ala Arg Arg Thr Gly Glu Ser Val Asp Leu
165 170 175
Gly Glu Leu Ile Phe Lys Leu Thr Lys Asn Val Ile Phe Arg Ala Ala
180 185 190
Phe Gly Ala Gly Ala Val Ala Ala Asp Ala Glu Glu Gly Asp Gly Ala
195 200 205
Gly Lys Gln Asp Glu Phe Ile Ala Ile Leu Gln Glu Phe Ser Lys Leu
210 215 220
Phe Gly Ala Phe Asn Ile Gly Asp Phe Ile Pro Trp Leu Ser Trp Ala
225 230 235 240
Asp Pro Gln Gly Ile Asn Val Arg Leu Arg Ala Ala Arg Asn Ala Leu
245 250 255
Asp Glu Phe Ile Asp Lys Ile Ile Asp Glu His Met Glu Arg Gly Lys
260 265 270
Asn Pro Asp Asp Ala Asp Ala Asp Met Val Asp Asp Met Leu Ala Phe
275 280 285
Leu Pro Glu Ala Lys Pro Lys Lys Gly Ala Ala Gly Asp Gly Val Asp
290 295 300
Asp Leu Gln Asn Thr Leu Arg Leu Thr Arg Asp Asn Ile Lys Ala Ile
305 310 315 320
Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile
325 330 335
Glu Trp Ala Met Ala Glu Met Met His Ser Pro Asp Asp Leu Arg Arg
340 345 350
Leu Gln Gln Glu Leu Val Asp Val Val Gly Leu Asp Arg Asn Val Asp
355 360 365
Glu Ser Asp Leu Asp Lys Leu Pro Phe Leu Lys Cys Val Ile Lys Glu
370 375 380
Thr Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala
385 390 395 400
Glu Asp Cys Val Val Gly Gly Tyr Ser Val Pro Arg Gly Ser Arg Val
405 410 415
Met Ile Asn Val Tyr Ala Ile Gly Arg Asp Arg Arg Ala Trp Lys Asp
420 425 430
Ala Asp Val Phe Arg Pro Ser Arg Phe Val Gln Gly Glu Gly Glu Ala

435 440 445
Ala Gly Leu Asp Phe Lys Gly Gly Cys Phe Glu Phe Leu Pro Phe Gly
450 455 460
Ser Gly Arg Arg Ser Cys Pro Gly Met Ala Leu Gly Leu Tyr Ala Leu
465 470 475 480
Glu Leu Ala Val Ala Gln Leu Ala His Gly Phe Ser Trp Glu Leu Pro
485 490 495
Asp Gly Met Lys Pro Ser Glu Leu Asp Met Ser Asp Val Phe Gly Leu
500 505 510
Thr Ala Pro Arg Ala Thr Arg Leu Phe Ala Val Pro Thr Pro Arg Leu
515 520 525
Ala Cys Thr Gln Leu Leu Gly Ala Asp Asp Ala Gly Arg Gln Ala
530 535 540

<210> 184
<211> 713
<212> PRT
<213> Festuca arundinacea

<400> 184
Met Glu Cys Glu Asn Gly His Val Ala Ala Asn Gly Asp Gly Leu Cys
1 5 10 15
Val Ala Gln Pro Ala Arg Ala Asp Pro Leu Asn Trp Gly Lys Ala Ala
20 25 30
Glu Glu Leu Ser Gly Ser His Leu Asp Ala Val Lys Arg Met Val Glu
35 40 45
Glu Tyr Arg Arg Pro Val Val Thr Met Glu Gly Ala Ser Leu Thr Ile
50 55 60
Ala Met Val Ala Ala Val Ala Ala Gly Ala Asp Thr Arg Val Glu Leu
65 70 75 80
Asp Glu Ser Ala Arg Gly Arg Val Lys Glu Ser Ser Asp Trp Val Met
85 90 95
Asn Ser Met Ala Asn Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe
100 105 110
Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln Arg
115 120 125
Glu Leu Ile Arg Phe Leu Asn Ala Gly Ala Phe Gly Thr Gly Ser Asp
130 135 140
Gly His Val Leu Pro Ala Ala Thr Thr Arg Ala Ala Met Leu Val Arg
145 150 155 160
Val Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu
165 170 175
Glu Thr Ile Ala Thr Leu Leu Asn Ala Asn Val Thr Pro Cys Leu Pro
180 185 190
Leu Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr
195 200 205
Ile Ala Gly Leu Val Thr Gly Arg Pro Asn Ser Val Ala Thr Ala Pro
210 215 220
Asp Gly Ser Lys Val Asn Ala Ala Glu Ala Phe Lys Ile Ala Gly Ile
225 230 235 240
Gln His Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Met Val
245 250 255
Asn Gly Thr Ala Val Gly Ser Gly Leu Ala Ser Ile Val Leu Phe Glu
260 265 270
Ala Asn Ile Leu Gly Ile Leu Ala Glu Val Leu Ser Ala Val Phe Cys
275 280 285
Glu Val Met Asn Gly Lys Pro Glu Tyr Thr Asp His Leu Thr His Lys
290 295 300
Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu His
305 310 315 320
Ile Leu Glu Gly Ser Ser Tyr Met Met Leu Ala Lys Lys Leu Gly Glu
325 330 335
Leu Asp Pro Leu Met Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr
340 345 350
Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ala Ala Thr
355 360 365

Lys Ser Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile
370 375 380
Asp Val Ser Arg Gly Lys Ala Ile His Gly Gly Asn Phe Gln Gly Thr
385 390 395 400
Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile
405 410 415
Gly Lys Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr
420 425 430
Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu
435 440 445
Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr Cys Ser
450 455 460
Glu Leu Gln Phe Leu Gly Asn Pro Val Thr Asn His Val Gln Ser Ala
465 470 475 480
Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ser Arg
485 490 495
Lys Thr Ala Glu Ala Ile Asp Ile Leu Lys Leu Met Ser Ser Thr Phe
500 505 510
Met Val Ala Leu Cys Gln Ala Ile Asp Leu Arg His Ile Glu Glu Asn
515 520 525
Val Lys Asn Ala Val Lys Asn Cys Val Lys Thr Val Ala Arg Lys Thr
530 535 540
Leu Ser Thr Asn Asp Ser Gly His Leu His Asn Ala Arg Phe Cys Glu
545 550 555 560
Lys Asp Leu Leu Leu Thr Ile Asp Arg Glu Ala Val Phe Ala Tyr Ala
565 570 575
Asp Asp Pro Cys Ser Ala Asn Tyr Pro Leu Met Gln Lys Met Arg Ala
580 585 590
Val Leu Val Glu His Ala Leu Ala Asn Gly Glu Ala Glu Gln Asp Val
595 600 605
Gln Thr Ser Val Phe Ala Lys Leu Ala Thr Phe Glu Gln Glu Leu Arg
610 615 620
Ala Val Leu Pro Lys Glu Val Glu Ser Ala Arg Cys Ser Val Glu Asn
625 630 635 640
Gly Thr Ala Ala Gln Gln Asn Arg Ile Ser Glu Cys Arg Ser Tyr Pro
645 650 655
Leu Tyr Arg Phe Val Arg Lys Glu Leu Gly Thr Glu Tyr Leu Thr Gly
660 665 670
Glu Lys Thr Arg Ser Pro Gly Glu Glu Val Asp Lys Val Phe Val Ala
675 680 685
Met Asn Gln Gly Lys His Ile Asp Ala Leu Leu Glu Cys Leu Lys Glu
690 695 700
Trp Asn Gly Glu Pro Leu Pro Ile Cys
705 710

<210> 185
<211> 324
<212> PRT
<213> Lolium perenne

<400> 185
Met Ala Pro Ala Thr Pro Lys Asp Ser Ser Ala Leu Pro Gly Leu Leu
1 5 10 15
Leu Leu Phe Ala Ala Ala Thr Ser Val Ala Val Ala Asn Ala Gln Leu
20 25 30
Ser Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu Thr Ile
35 40 45
Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met Gly Ala
50 55 60
Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp
65 70 75 80
Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu Lys Gly
85 90 95
Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile Asp Lys
100 105 110
Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser Cys Ala

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        115                 120                 125
Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu Gly Gly
    130                 135                 140
Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr Ala Ser
145                 150                 155                 160
Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn Leu Asn
                165                 170                 175
Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr Asp Met
            180                 185                 190
Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys Gln Asn
        195                 200                 205
Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala Phe Ala
    210                 215                 220
Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly Asn Leu
225                 230                 235                 240
Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly Tyr Phe
                245                 250                 255
Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln Ala Leu
            260                 265                 270
Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala Ser Asn
        275                 280                 285
Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Ala Met Val Lys Leu Ser
    290                 295                 300
Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val Asn Cys
305                 310                 315                 320
Arg Ala Val Asn


<210> 186
<211> 398
<212> PRT
<213> Lolium perenne

<400> 186
Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
 1               5                  10                  15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
            20                  25                  30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
        35                  40                  45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
    50                  55                  60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
65                  70                  75                  80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
                85                  90                  95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
            100                 105                 110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
        115                 120                 125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
    130                 135                 140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
145                 150                 155                 160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
                165                 170                 175
Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
            180                 185                 190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
        195                 200                 205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
    210                 215                 220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
225                 230                 235                 240
Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
                245                 250                 255
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```
Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
            260                 265                 270
Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
        275                 280                 285
Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
    290                 295                 300
Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
305                 310                 315                 320
Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
                325                 330                 335
Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
            340                 345                 350
Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
        355                 360                 365
Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
    370                 375                 380
Val Val Leu His Ser Met Pro Ile Ala Ala Asp Ala Thr Ala
385                 390                 395
```

<210> 187
<211> 370
<212> PRT
<213> Festuca arundinacea

<400> 187

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Met Lys Gln Glu Val Lys Ser Glu Met Asn Gly Glu Thr Met Ser Gly
 1               5                  10                  15
Asn Lys Gly Pro Val Val Val Thr Gly Ala Ser Gly Phe Val Gly Ser
            20                  25                  30
Trp Leu Val Met Lys Leu Leu Gln Ala Gly Tyr Thr Val Arg Ala Thr
        35                  40                  45
Val Arg Asp Pro Gly Asn Val Glu Lys Thr Lys Pro Leu Leu Glu Leu
    50                  55                  60
Pro Gly Ala Lys Glu Arg Leu Ser Ile Trp Arg Ala Asp Leu Ser Glu
65                  70                  75                  80
Glu Gly Ser Phe Asp Glu Ala Ile Ala Gly Cys Thr Gly Val Phe His
                85                  90                  95
Val Ala Thr Pro Met Asp Phe Glu Ser Lys Asp Pro Glu Asn Glu Val
            100                 105                 110
Ile Lys Pro Thr Val Glu Gly Met Leu Ser Ile Met Arg Ala Cys Lys
        115                 120                 125
Glu Ala Gly Thr Val Lys Arg Val Val Phe Thr Ser Ser Ala Gly Thr
    130                 135                 140
Val Asn Ile Glu Glu Arg Pro Arg Pro Ala Tyr Asp Gln Asp Asn Trp
145                 150                 155                 160
Ser Asp Ile Asp Phe Cys Arg Arg Val Lys Met Thr Gly Gln Met Tyr
                165                 170                 175
Phe Val Ser Lys Ser Leu Ala Glu Lys Ala Ala Met Asp Tyr Ala Lys
            180                 185                 190
Glu Asn Gly Val Asp Phe Ile Ser Ile Ile Pro Thr Leu Val Val Gly
        195                 200                 205
Pro Phe Leu Ser Ala Gly Met Pro Pro Ser Leu Val Thr Ala Leu Ala
    210                 215                 220
Leu Ile Thr Gly Asn Glu Ala His Tyr Ser Ile Leu Lys Gln Val Gln
225                 230                 235                 240
Leu Val His Leu Asp Asp Leu Cys Asp Ser Met Thr Tyr Leu Phe Glu
                245                 250                 255
His Pro Asp Ala Asn Gly Arg Tyr Ile Cys Ser Ser His Asp Thr Thr
            260                 265                 270
Ile His Gly Ile Ala Arg Met Leu Lys Glu Arg Phe Pro Glu Tyr Asp
        275                 280                 285
Ile Pro Gln Lys Phe Pro Gly Val Asp Asp Asp Leu Gln Pro Ile His
    290                 295                 300
Phe Phe Phe Lys Lys Leu Leu Asp His Gly Phe Arg Phe Arg Tyr Thr
305                 310                 315                 320
Ala Glu Asp Met Phe Asp Ala Ala Val Trp Thr Cys Arg Glu Lys Gly
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325 330 335
Leu Ile Pro Leu Gly Ala Glu Gly Ala Gly Gly Pro Ala Ser Ala Ala
340 345 350
Gly Lys Leu Gly Ala Val Leu Val Gly Glu Gly Gln Ala Ile Gly Ala
355 360 365
Glu Thr
370

<210> 188
<211> 329
<212> PRT
<213> Lolium perenne

<400> 188
Met Ala Thr Glu Ala Lys Gly Glu Thr Val Leu Val Thr Gly Ala Ser
1 5 10 15
Gly Phe Ile Gly Ser Trp Leu Val Arg Leu Leu Leu Ala Arg Gly Tyr
20 25 30
Ser Val His Ala Ala Val Leu Asn Pro Asp Asp Lys Ala Glu Thr Asp
35 40 45
His Leu Leu Ala Leu Ala Ala Ala Ala Gly Asp Glu Gly Arg Ile Arg
50 55 60
Phe Phe Arg Cys Asp Leu Leu Asp Gly Ala Ala Met Leu Ala Ala Val
65 70 75 80
Arg Gly Cys Ser Gly Val Phe His Leu Ala Ser Pro Cys Thr Val Asp
85 90 95
Leu Val Leu Asp Pro Gln Lys Glu Leu Val Val Pro Ala Val Glu Gly
100 105 110
Thr Leu Asn Val Leu Arg Ala Ala Lys Glu Ala Gly Gly Val Arg Arg
115 120 125
Val Val Val Thr Ser Ser Val Ser Ala Leu Val Pro Cys Pro Gly Trp
130 135 140
Pro Ala Gly Glu Val Leu Asp Glu Arg Cys Trp Thr Asp Ile Asp Tyr
145 150 155 160
Cys Asp Lys Asn Gly Val Trp Tyr Pro Ala Ser Lys Ala Leu Ala Glu
165 170 175
Lys Ala Ala Trp Lys Phe Ala Glu Glu Asn Gly Leu Asp Val Val Thr
180 185 190
Val Asn Pro Gly Thr Val Leu Gly Glu Met Ile Pro Pro Arg Leu Asn
195 200 205
Ala Ser Met Ala Met Phe Leu Arg Leu Leu Glu Gly Cys Lys Glu Glu
210 215 220
Tyr Ala Asp Phe Phe Ile Gly Pro Val His Val Glu Asp Val Ala Leu
225 230 235 240
Ala His Ile Leu Leu Tyr Glu Asn Pro Ser Ala Ser Gly Arg His Leu
245 250 255
Cys Val Glu Pro Ile Cys His Trp Ser Val Phe Ala Ala Lys Val Ala
260 265 270
Glu Leu Tyr Pro Asp Tyr Lys Val Pro Lys Phe Pro Glu Asp Thr Gln
275 280 285
Pro Gly Leu Val Arg Ala Glu Ala Val Pro Lys Lys Leu Met Ala Leu
290 295 300
Gly Leu Gln Phe Thr Pro Leu Glu Lys Ile Ile Arg Asp Ala Val Glu
305 310 315 320
Ser Leu Lys Ser Arg Gly Cys Ile Ala
325

<210> 189
<211> 330
<212> PRT
<213> Lolium perenne

<400> 189
Met Val Ser Ser Thr Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly
1 5 10 15
Phe Val Ala Ser Trp Leu Ile Lys Lys Leu Leu Glu Ser Gly Tyr His

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                20                  25                  30
Val Ile Gly Thr Val Arg Asp Pro Gly Asn Arg Arg Lys Val Gly His
        35                  40                  45
Leu Trp Lys Leu Pro Gly Ala Asn Glu Arg Leu Gln Leu Val Arg Ala
    50                  55                  60
Asp Leu Leu Glu Glu Gly Ser Phe Asp Asp Ala Val Arg Ala Cys Glu
65                  70                  75                  80
Gly Val Phe His Ile Ala Ser Pro Val Leu Gly Lys Ser Asp Ser Asn
                85                  90                  95
Cys Lys Glu Ala Thr Leu Gly Pro Ala Ile Asn Gly Thr Leu Asn Val
            100                 105                 110
Leu Arg Ser Cys Lys Lys Ser Pro Phe Leu Lys Arg Val Val Leu Thr
        115                 120                 125
Ser Ser Ser Ser Ala Val Arg Ile Arg Asp Glu Thr Gln Gln Pro Glu
    130                 135                 140
Leu Leu Trp Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys
145                 150                 155                 160
Leu Gln Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala
                165                 170                 175
Leu Asp Phe Ala Lys Glu Asn Asn Ile Asp Leu Val Thr Val Leu Pro
            180                 185                 190
Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Thr Thr Ala
        195                 200                 205
Ser Asp Ile Leu Gly Leu Leu Gln Gly Asp Thr Asp Arg Phe Thr Leu
    210                 215                 220
Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Arg Ser His
225                 230                 235                 240
Ile Leu Val Tyr Glu Thr Pro Glu Ala Thr Gly Arg Tyr Leu Cys Ser
                245                 250                 255
Ser Val Val Leu Asp Asn Asn Glu Leu Val Gly Leu Leu Ala Lys Gln
            260                 265                 270
Phe Pro Val Phe Pro Ile Pro Arg Arg Leu Lys Asn Pro Tyr Gly Lys
        275                 280                 285
Gln Ala Tyr Gln Leu Asp Thr Ser Lys Leu Gln Gly Leu Gly Leu Lys
    290                 295                 300
Phe Lys Gly Val Gln Glu Met Phe Asn Asp Cys Val Glu Ser Leu Lys
305                 310                 315                 320
Asp Gln Gly His Leu Leu Glu Cys Pro Leu
                325                 330
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<210> 190
<211> 326
<212> PRT
<213> Lolium perenne

<400> 190

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Met Ala Pro Ala Thr Pro Lys Asp Ser Ser Ser Ser Ala Leu Pro Gly
1               5                   10                  15
Leu Leu Leu Leu Leu Ala Ala Ala Thr Ser Val Ala Val Ala Asn Ala
            20                  25                  30
Gln Leu Ser Glu Asn Tyr Tyr Gly Ser Ser Cys Pro Thr Ala Leu Leu
        35                  40                  45
Thr Ile Arg Thr Val Val Thr Thr Ala Val Leu Leu Asp His Arg Met
    50                  55                  60
Gly Ala Ser Leu Leu Arg Leu His Phe His Asp Cys Phe Val Gln Gly
65                  70                  75                  80
Cys Asp Ala Ser Val Leu Leu Asp Asp Thr Ala Gly Phe Thr Gly Glu
                85                  90                  95
Lys Gly Ala Gly Pro Asn Ala Gly Ser Leu Arg Gly Leu Glu Val Ile
            100                 105                 110
Asp Lys Ile Lys Met Leu Leu Glu Phe Met Cys Pro Arg Thr Val Ser
        115                 120                 125
Cys Ala Asp Ile Leu Ala Val Ala Ala Arg Asp Ser Val Val Arg Leu
    130                 135                 140
Gly Gly Pro Ser Trp Ala Val Gln Leu Gly Arg Arg Asp Ala Thr Thr
145                 150                 155                 160
```

```
Ala Ser Ala Ser Leu Ala Ser Ser Asp Leu Pro Gly Pro Asn Ser Asn
                165                 170                 175
Leu Asn Asp Leu Leu Thr Ala Phe Ser Lys Lys Gly Leu Ser Thr Thr
            180                 185                 190
Asp Met Val Ala Leu Ser Gly Ala His Thr Ile Gly Arg Ala Gln Cys
        195                 200                 205
Gln Asn Tyr Arg Asn Arg Ile Tyr Thr Asp Thr Asp Ile Asp Gly Ala
    210                 215                 220
Phe Ala Ala Ser Leu Arg Gly Gly Cys Pro Gln Ala Gly Gly Asp Gly
225                 230                 235                 240
Asn Leu Ala Pro Leu Asp Ala Ser Ser Pro Asn Thr Phe Asp Asn Gly
                245                 250                 255
Tyr Phe Ser Gly Leu Leu Ser Arg Gln Gly Leu Leu His Ser Asp Gln
            260                 265                 270
Ala Leu Tyr Asp Gly Gly Ser Thr Asp Asp Leu Val Arg Thr Tyr Ala
        275                 280                 285
Ser Asn Asn Asp Gln Phe Gly Ser Asp Phe Ala Ala Ala Met Val Lys
    290                 295                 300
Leu Ser Asn Ile Gly Leu Leu Thr Gly Ser Ser Gly Glu Ile Arg Val
305                 310                 315                 320
Asn Cys Arg Ala Val Asn
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<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 191
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<210> 192
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 192
cggtagagat ccagtctaga g 21

<210> 193
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 193
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<210> 194
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<400> 194
ccacggctaa ctaatggttc a 21

<210> 195
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<210> 197
<211> 18
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<400> 198
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<210> 199
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<220>
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<400> 199
tcatgacgat tccaagaacg 20

<210> 200
<211> 19
<212> DNA
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<220>
<223> Made in the lab

<400> 200
gttgaccgtg actcgtcgt 19

<210> 201
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 201
actgaattct cggtcccagc ctccatt 27

<210> 202
<211> 29
<212> DNA
<213> Artificial Sequence

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<223> Made in the lab

<400> 202
gtagcggccg cgcgaaaact cgtcggaga 29

<210> 203
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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<400> 203
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<210> 204
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<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 204
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<210> 205
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 205
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<210> 206
<211> 27
<212> DNA
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<223> Made in the lab

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atgcggccgc gcaacatgct agcacaa 27

<210> 207
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ggtcgtagaa ggacttgg 18

<210> 209
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<220>
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<400> 209
cgccttcatc ttcaagac 18

<210> 210
<211> 17
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<400> 210
agccctggcg taaatgg 17

<210> 211
<211> 20
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<213> Artificial Sequence

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<400> 211
gacgcaagga gagatccaga 20

<210> 212
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<400> 212
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<210> 214
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<400> 214
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gtggacatgg accagaaggt 20

<210> 218
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cggtacatct cggtgaaggt 20